

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R40-3-40B2-IR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--
R40-4-40B12-IR	IRDMHYVWQDRDRYINGVRQWYISDRYNPGSAFYRWFD	40.3	9.0	2.0	4.5
R40-4-40G11-IR	RMGLQALAHYRKSAGPIFLSSGSVIKGSEGDPPFYAWFRLQ	60.4	12.9	2.0	6.5
	MPVSLFRRVWDYRDGEHETLESHYVVPQAALDRLFYSWFS	52.6	37.5	2.0	18.8
					0.1

Figure 1A

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R40-3-D5-IGFR	PLYGGGIHLYPGTMGYVPGFPRQVKVLGDADKNFYDWF	--	--	--	--	--
R40-3-A6-IGFR	YRGLVLGRISDGAGKVASEPPIQKVFVAFNYDFV	--	--	--	--	--
R40-X-R35-IGFR	SGCCRLGLRWMFIVVWWSGALVCQSAASAAGFYDWF	--	--	--	--	--

Figure 1B

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20α-3-20D3-IR	IGGGQHGDGNFYDWFVEALA	46.3	36.2	7.0	5.2	0.2
R20α-3-20F1-IR	VFWNCRSQQLDFYEWFEQAA	49.0	26.0	2.8	9.3	0.1
R20α-3-20H1-IR	RVAGAISAPGLVSNKQDGLFYSWFRE	45.6	35.3	3.3	10.7	0.1
R20α-3-20D1-IR	VLQARHGCDSSVDCFYEWFA	50.8	37.5	3.0	12.5	0.1
R20β-4-B12-IR	GAFYRWFHEALVGSERVDPV	41.9	2.9	5.7	0.5	2.0
R20β-4-H3-IR	HEAFYDWFSAIVDGGYELMG	13.9	5.8	2.4	2.4	0.4
R20β-4-D10-2-IR	RIGGGWARSEGIFYEWFVREL	21.5	7.3	2.9	2.5	0.4
R20β-4-C8-IR	LPAGGA?GFA?RGFYEWFES	44.9	31.1	9.6	3.2	0.3
R20β-4-E7-IR	GHSWALVRHVDRLFYEWFDL	45.0	18.8	5.9	3.2	0.3
R20β-4-E7-2-IR	LGTSAGQGVGHRAFYQWFQS	45.0	18.8	5.9	3.2	0.3
R20β-4-G3-IR	RGGGTFYEWFPESALRKHGAG	38.6	7.5	2.0	3.8	0.3
R20β-4-H6-IR	NSSGQVVGTLTFYSWFASQV	14.8	7.6	2.0	3.8	0.3
R20β-4-G11-IR	FYGWFSRQLSLTPRDDWGLP	39.4	7.5	1.9	3.9	0.3
R20β-4-G8-IR	RMFYEWFSQMAGPTEGSA	41.2	15.1	3.4	4.4	0.2
R20β-4-H9-IR	IGGGQHGDGNFYDWFVEALA	43.1	8.8	2.0	4.4	0.2
R20β-4-H8-IR	RDKPTDQEEQNWSFYEWFRH	47.9	43.7	9.3	4.7	0.2
R20β-4-B8-IR	WSALLSVMDTGFYAWFDDAV	44.0	40.1	8.4	4.8	0.2
R20β-4-E2-IR	SRDQTNFTFNSAGFYGWFER	16.3	13.9	2.4	5.8	0.2
R20β-4-F4-IR	GVGTLTMSSDAFYTWfV	15.3	5.9	1.0	5.9	0.2
R20β-4-A8-IR	IGGSFVEFYGWFNQDV	43.3	36.0	6.0	6.0	0.2
R20β-4-C4-IR	DIGSDGHGRRWDSFYRWfEM	17.3	26.8	4.3	6.2	0.2
R20β-4-D7-IR	VLQARHGCDSSVDCFYEWFA	44.8	36.2	5.6	6.5	0.2
R20β-4-D2-IR	DPERMQSDVGfYEWfRAAVG	31.2	29.4	2.9	10.1	0.1

Figure 1C

423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R20-4-B9-IGFR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
R20-4-F8-IGFR	DPERMQSDVGFYEWFRRAAVG	40.1	16.6	--	--
R20-4-G12-IGFR	DIGSDGHGRRWDSFYRWFEM	39.2	13.9	--	--
R20-4-D10-IGFR	PFYQWFLDQSVGSGRGGGLR	36.7	8.0	--	--
	AVAPLSVRGRDSGFYSWFSS	40.2	4.1	--	--

Figure 1D

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFSR	IR	IGFSR/IR	IR/IGFSR
A6S-3-E12-IR	XXXXXXXXXXNFYDWFVXXXX	26.2	1.3	8.0	0.2	6.2
A6S-2-C1-IR	GRVDWLQRNANFYDWFVAELG	41.2	1.3	7.0	0.2	5.4
A6S-1-A7-IR	RMVFSTGAPQNFYDWFVQEW	47.2	2.3	11.1	0.2	4.8
A6S-2-C8-IR	HHTQGLQVQRNFYDWFVNELR	44.9	1.5	5.5	0.3	3.7
A6S-3-E10-IR	MHRMQHDGTSNFYDWFVLQWA	46.9	1.6	5.0	0.3	3.1
A6S-2-D5-IR	AMHVVAQGGPNFYDWFVREL	31.9	1.2	3.7	0.3	3.1
A6S-1-B2-IR	AIQMNGLAFNFYDWFVRELT	31.6	1.8	5.3	0.3	2.9
A6S-1-A4-IR	TDRKSVQEPNRYDWFVWAAR	43.3	3.6	9.2	0.4	2.6
A6S-4-G3-IR	PHGHRGFAQSNFYDWFVTQEE	31.3	2.3	5.1	0.5	2.2
A6S-4-H8-IR	RLASASVPGQNFYDWFVDQLL	11.5	1.7	3.6	0.5	2.1
A6S-3-E11-IR	RQSEFSTLNSNFYDWFVRELE	26.3	2.3	4.4	0.5	1.9
A6S-1-A1-IR	GQAQLSIRDVNFYDWFVQQLV	36.9	3.7	6.5	0.6	1.8
A6S-2-C9-IR	MSEPAVGVNGNFYDWFVAQLF	43.6	1.3	2.3	0.6	1.8
A6S-2-C4-IR	VTGRARLDRNFYDWFVGQYS	34.5	5.6	9.6	0.6	1.7
A6S-4-H10-IR	SREAVQKRNFYDWFVQQLS	39.2	4.4	6.9	0.6	1.6
A6S-4-G7-IR	LAQFAGSRNQNFYDWFVEQLG	19.1	1.4	2.2	0.6	1.6
A6S-4-H2-IR	GQEYFDQMGLNFYDWFVRELD	25.5	2.6	3.9	0.7	1.5
A6S-2-C3-IR	RQPSQPPHGSNFYDWFVEAIN	31.1	1.6	2.4	0.7	1.5
A6S-2-C11-IR	LMQSLGSGSTNFYDWFVQQMV	20.9	3.3	4.6	0.7	1.4
A6S-3-F3-IR	DQORSACDGTNFYDWFVCQLS	37.1	3.0	4.2	0.7	1.4
A6S-3-E5-IR	LDGTKACQRVNFYDWFVCQTE	31.6	2.5	3.5	0.7	1.4
A6S-1-B7-IR	PEARRTVVHSNFYDWFVAQLS	49.2	1.6	2.3	0.7	1.4
A6S-3-E7-IR	PWMLSVGIQDNFYDWFVGLDS	37.2	5.0	6.3	0.8	1.3
A6S-4-G6-IR	ASHQRGSSDNFYDWFVAQMR	16.8	3.1	4.0	0.8	1.3
A6S-2-C2-IR	TLEREGEFSGNFYDWFVEQLH	29.7	2.4	3.1	0.8	1.3
A6S-3-F1-IR	DRQSIGSVHGDYDWFVSALG	29.7	2.3	3.0	0.8	1.3
A6S-2-C5-IR	DWDKLGSLSENFYDWFVDQLA	42.9	6.1	7.0	0.9	1.1
A6S-3-E4-IR	VRVVLNQSGRNFYDWFVIOLE	20.9	2.1	2.3	0.9	1.1
	MASWQSRTPDNFYDWFVRELS					

Figure 1E

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
A6S-3-E9-IR	XXXXXXXNFYDFVXXXX	36.6	9.0	8.9	1.0 1.0
A6S-3-E1-IR	TTCHPRGEDCNFYDFVQLR	36.7	6.8	6.9	1.0 1.0
A6S-4-H12-IR	VRGNDVLRANFYDFVQDLS	46.3	6.1	5.8	1.1 1.0
A6S-2-D3-IR	TPRSQVRSDHNFYDFVYQLA	37.0	5.3	5.1	1.0 1.0
A6S-3-E8-IR	ESLTGSRPDRNFYDFVQOTS	42.7	5.2	5.1	1.0 1.0
A6S-1-A12-IR	PQSLTEVRTGNFYDFVQQLH	39.7	2.1	2.1	1.0 1.0
A6S-4-H3-IR	DVGMGRVKETNFYDFVQRLI	18.6	3.1	2.9	1.1 0.9
A6S-3-F7-IR	GADDIRSLTNFYDFVFNQLS	46.2	2.3	2.1	1.1 0.9
A6S-2-D8-IR	GVSIQAGYKTNFYDFVFEAVR	31.2	2.0	1.7	1.2 0.9
A6S-3-F10-IR	VGEHRQMSVGNFYDFVQMIA	39.0	5.9	4.5	1.3 0.8
A6S-4-G11-IR	GSSLGRSGPCNFYDFVQDLE	44.8	4.3	3.3	1.3 0.8
A6S-2-D2-IR	HRQQDVVRQGNFYDFVQALE	33.5	3.6	2.7	1.3 0.8
A6S-4-G8-IR	QDTFLTAREGNFYDFVIRALE	11.1	2.5	1.9	1.3 0.8
A6S-4-H6-IR	EAIMREEQANFYDFVVRQLE	22.4	2.4	1.9	1.3 0.8
A6S-2-D10-IR	VCDVSTGGTNFYDFVVCQVG	41.3	2.1	1.7	1.2 0.8
A6S-3-F4-IR	PQPRSASTPLNFYDFVQATG	37.0	13.5	9.9	1.4 0.7
A6S-4-G9-IR	GVSRRGGDPNFYDFVVMQLR	36.2	11.8	7.8	1.5 0.7
A6S-3-F5-IR	GPGRHDSSRGNFYDFVEQLA	48.1	7.2	4.8	1.5 0.7
A6S-4-H1-IR	ERFALEVQGSNFYDFVVRQVI	18.3	3.6	2.6	1.4 0.7
A6S-3-F6-IR	NLKSSATVGGNFYDFVFEQL	18.7	2.9	1.9	1.5 0.7
A6S-3-F11-IR	MEGPPAGGPLNFYDFVQVD	33.8	2.0	1.4	1.4 0.7
A6S-2-C6-IR	RLDVAGHRGGNFYDFVKQLH	46.7	19.2	12.1	1.6 0.6
A6S-4-G4-IR	PWSDHEALNQNFYDFVVSQVL	36.9	18.2	10.7	1.7 0.6
A6S-4-G12-IR	EDRLNGESTNFYDFVVRQLA	32.8	12.8	7.9	1.6 0.6
A6S-2-D7-IR	GKLVASTLDDNFYDFVVRQLS	33.2	12.0	7.1	1.7 0.6
A6S-4-G10-IR	SGPVVQTQNGNFYDFVHQLR	33.9	10.8	6.8	1.6 0.6
A6S-3-F9-IR	VDRAGPAGSDNFYDFVQALD	44.3	9.6	5.7	1.7 0.6
A6S-3-F2-IR	SLGRNDRPDENFYDFVVSQVQ	23.2	4.3	2.5	1.7 0.6
	RVMATANAPMNFYDFVQQLQ				

Figure 1E (Con't)

Clone	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
Design	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--	--	
A6S-4-G1-IR	NGVERAGTDGNFYDWFVAQLH	36.2	31.8	15.7	2.0	0.5	
A6S-1-A3-IR	PFAGKGDKTGNFYDWFVSLTG	39.9	12.6	6.0	2.1	0.5	
A6S-3-F12-IR	GMPQEYMDQNVNFYDWFVAQVD	41.4	7.4	4.0	1.9	0.5	
A6S-4-G2-IR	MGTPAVGDGANFYDWFVRQLG	26.7	7.0	3.5	2.0	0.5	
A6S-1-B1-IR	SKCKAWYGANNFYDWFVWQVD	30.6	3.7	1.9	1.9	0.5	
A6S-2-D11-IR	EAASLGSQDRNFYDWFVRQVV	48.4	37.4	13.5	2.8	0.4	
A6S-2-D1-IR	VERSASSQDGNFYDWFVVQIR	37.8	30.6	12.0	2.6	0.4	
A6S-3-E2-IR	TSEVQRRSQDGNFYDWFVAQVA	33.1	24.7	9.8	2.5	0.4	

Figure 1E (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6S-4-E4-IGFR	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--	--
A6S-2-D2-IGFR	ERSAAGFREGNFYDWFVAQVN	27	32	--	--	--
A6S-2-F2-IGFR	RAERGSMRDSNFYDWFVQQLP	36	30	--	--	--
A6S-4-F3-IGFR	LAMSVASRPANFYDWFVAQIV	35	30	--	--	--
A6S-4-G4-IGFR	HNSSSPMRTGNFYDWFVQELR	26	30	--	--	--
A6S-4-G3-IGFR	SALSGPVQPINFYDWFVTGM	26	30	--	--	--
A6S-2-H2-IGFR	GAQAIREIHNFYDWFVAQVT	21	29	--	--	--
A6S-2-E3-IGFR	RQRESDSGTNFYDWFVGAIR	40	28	--	--	--
A6S-4-C6-IGFR	VQEGLSGMEGNFYDWFVDQLF	36	28	--	--	--
A6S-4-F5-IGFR	RLDRSSTSGVNFYDWFVAQVG	25	28	--	--	--
A6S-4-H3-IGFR	GSQHSGREPHNFYDWFVAQVG	24	28	--	--	--
A6S-4-H4-IGFR	GRDQRHETTTFYDWFVRELQ	20	28	--	--	--
A6S-2-H1-IGFR	PRMVEKPSEDNFYDWFVTQLS	20	28	--	--	--
A6S-4-E6-IGFR	RVGIQVDPHTNFYDWFVIQLT	42	27	--	--	--
A6S-4-B6-IGFR	RSSGGLLSQGNFYDWFVSQLE	24	26	--	--	--
A6S-4-D2-IGFR	SDARQAGLQENFYDWFVSQVR	23	26	--	--	--
A6S-4-G5-IGFR	PPYRSRLGENFYDWFVMQVR	19	26	--	--	--
A6S-2-A3-IGFR	QEVTRTRDDKNFYDWFVSQIF	18	26	--	--	--
A6S-4-E2-IGFR	SRAPYCGTAGNFYDWFVQAVS	37	25	--	--	--
A6S-4-G6-IGFR	?DQGSVSSKGNFYDWFVQQMT	25	25	--	--	--
A6S-4-D6-IGFR	RLMGGIAEPQNFYDWFVREVA	20	25	--	--	--
A6S-4-F4-IGFR	SAGHHMPRESNFYDWFVDQVV	25	24	--	--	--
A6S-4-C3-IGFR	LGAETWDGINFYDWFVKQVS	22	24	--	--	--
A6S-4-H5-IGFR	VHSGVPPYPNFYDWFVMQVS	22	24	--	--	--
A6S-4-H6-IGFR	VTMLDKGAQDNFYDWFVREVA	21	24	--	--	--
A6S-4-F6-IGFR	HHSPGNEHGYNFYDWFVLQVA	19	24	--	--	--
A6S-3-H1-IGFR	GSIACLIMRANFYDWFVEQTN	18	24	--	--	--
	LKGSSQPLSVNFYDWFVQQIK	17	24	--	--	--
	PASNKNSLAENFYDWFVQQTR	30	23	--	--	--

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Ratios over Background		Sequence	Comparisons		IR	IGFR/IR	IR/IGFR
Clone	Design		E-Tag	IGFsR			
A6S-1-D5-IGFR	A6S-1-D5-IGFR	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--	--
A6S-1-A2-IGFR	A6S-1-A2-IGFR	RVSGMEDLGNFYDWFVRQAQ	25	5	--	--	--
A6S-3-E6-IGFR	A6S-3-E6-IGFR	KDPVTVSQGRNFYDWFVQIQ	20	5	--	--	--
A6S-1-G3-IGFR	A6S-1-G3-IGFR	DARDHGVWMSNFYDWFVAQVS	20	5	--	--	--
A6S-3-G4-IGFR	A6S-3-G4-IGFR	VATVHVGGGMNFYDWFVAQVG	19	5	--	--	--
A6S-3-H8-IGFR	A6S-3-H8-IGFR	CADPGACSSLNFYDWFVQMRG	21	4	--	--	--
A6S-3-E3-IGFR	A6S-3-E3-IGFR	NPTSVQQYGVNFYDWFVNVLS	20	4	--	--	--
A6S-3-D9-IGFR	A6S-3-D9-IGFR	RPSLPEVRPGNFYDWFVQSVR	19	4	--	--	--
A6S-2-A1-IGFR	A6S-2-A1-IGFR	SLQGADFQQGNFYDWFVSELA	17	4	--	--	--
A6S-1-H4-IGFR	A6S-1-H4-IGFR	LSSRGRVTMRNFYDWFVAQVV	31	3	--	--	--
A6S-3-C1-IGFR	A6S-3-C1-IGFR	HKSWTTMSPLNFYDWFVAQVE	18	3	--	--	--
A6S-3-B10-IGFR	A6S-3-B10-IGFR	RPVIGGGGTRNFYDWFVAQMI	17	3	--	--	--
		YDQDPPYWGLNFYDWFVREVA	16	3	--	--	--

Figure 1F (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-D1-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	19.0	4.0	--	--	--
A6L-4-H7-IR		QRGMLVRGRISHGAGKIAIEPPDCLGQKACAVNFYDWFV	22.6	19.8	26.5	0.7	1.3
A6L-4-H4-IR		QRGMLLLGRISDDAGKVASEPSARRGQKVFAFNFYDWFV	37.5	3.5	4.2	0.8	1.2
A6L-4-E4-IR		YRGILVLGRISSEGAGKVASEPAARIGQKVFAFNFYDWFV	38.5	21.1	25.8	0.8	1.2
A6L-4-G7-IR		QRCMLALGRISDGAGKVASEPPAGIGQKVFAFNFYDWFV	38.1	5.4	6.0	0.9	1.1
A6L-3-C3-IR		FRGRLVLGHFSDGAGKVSEPAARIGQKVFDVNFYDWFV	38.6	16.2	18.5	0.9	1.1
A6L-3-B6-IR		YRGMLVLGRISDGAGKVASEPPARIGQEVFADNFYDWFV	34.7	21.8	23.1	0.9	1.1
A6L-4-G11-IR		YRGMLVLGRISDGAGEVASEPPARIGQEVFALNFYDWFV	33.1	27.8	30.3	0.9	1.1
A6L-4-G12-IR		VPWYAGSGSSSDGAGKVASEPPARIDQKVFAVNFYDWFV	27.6	2.0	2.0	1.0	1.0
A6L-3-A10-IR		YRGQLVLGRISYGAGKVGCDPPARIGQKDWAVNFYDWFV	32.0	2.3	2.3	1.0	1.0
A6L-4-E12-IR		QRLGLVLGRFSDGAGNVASEPPAGIGQEVFPVNFYDWFV	21.1	2.4	2.4	1.0	1.0
A6L-4-E10-IR		QRCMLVLGRISDGAGKVAEPPDCLGQKVCANFYDWFV	3.1	2.4	2.4	1.0	1.0
A6L-4-G8-IR		QRCMLVLGRISDGAGKVAESELPPRIGQKDFAVNFYDWFV	30.1	3.8	3.8	1.0	1.0
A6L-3-C12-IR		QRCMLVLGRISDGAGKVAEAPARIGQTVFAVNFYDWFV	37.9	4.7	4.7	1.0	1.0
A6L-4-H11-IR		QPCAGSGRIYDGACKVASEPPAHIGQEVFAVNFYDWFV	29.5	5.7	5.7	1.0	1.0
A6L-4-F10-IR		QRCMLVLDRISDGAGKVASGPPPARIGQNVLA VNFYDWFV	35.4	9.6	9.6	1.0	1.0
A6L-4-E9-IR		YRGMLVVGRIISDGTGKVASQPPPARIGQKVFAVNFYDWFV	31.6	10.5	10.5	1.0	1.0
A6L-4-H8-IR		YRGMLVLGRISDGAGKVASVPPAHIGQKVFAFNFYDWFV	39.8	12.9	12.9	1.0	1.0
A6L-3-A11-IR		QHGMLVLGRVSVGAGKVPSEPPARIGHKVDVNFYDWFV	38.2	14.6	14.6	1.0	1.0
A6L-4-F9-IR		YSGYAGSGSFDGAGKVASEPPARISQEVLA DNFYDWFV	29.0	17.5	17.5	1.0	1.0
A6L-4-G2-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVSANFYDWFV	35.7	18.4	18.4	1.0	1.0
A6L-4-E8-IR		YHGKLDLGRISVGVGKVAEPPPARIGQKVFA DNFYDWFV	29.5	21.4	20.7	1.0	1.0
A6L-4-H10-IR		YRGQAGSGVSLTVAGKVADPPPARIGQKVFA DNFYDWFV	28.7	21.6	21.6	1.0	1.0
A6L-4-G9-IR		HRGMLVLGRISSEGAGNVDPPEPPARIGQNVFA GNFYDWFV	30.0	22.1	22.1	1.0	1.0
A6L-4-F7-IR		QRCMPVLGRISDGAGKVGSEPPARIARKVFPVNFYDWFV	37.1	22.6	22.6	1.0	1.0
A6L-4-E11-IR		QGGLLVTGRISDGAGKVASEPPGGIGQKVFA GNFYDWFV	28.6	23.6	24.4	1.0	1.0
		YPWYGGSGTYLDGAGKVASEPPARIDQQVFA GNFYDWFV	38.4	26.5	26.5	1.0	1.0

Figure 1C

Clone	Parental/Design	Sequence	Rates over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-4-H9-IR	YRGLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	YRGLVLGRISDVAGIVDSEPPTRIGQKVFAGNFYDWFV	19.0	4.0	--	--	--
A6L-4-E1-IR	YRGLVLGRISQAGNVASEPSSRIGQKVFAGNFYDWFV	YRGLVLGRISQAGNVASEPSSRIGQKVFAGNFYDWFV	37.5	27.3	27.3	1.0	1.0
A6L-3-A5-IR	YRGLVLGRISDGAGKVDYEPARIGQKVFAGNFYDWFV	YRGLVLGRISQAGNVASEPSSRIGQKVFAGNFYDWFV	35.4	32.6	31.4	1.0	1.0
A6L-4-G4-IR	YRGLGLGGSAGAGIVASEPPARVGQKVFAGNFYDWFV	YRGLVLGRISDGAGKVDYEPARIGQKVFAGNFYDWFV	38.3	34.6	35.5	1.0	1.0
A6L-4-H2-IR	YRGILFQGRIPDGAGKVASEPPTRIGERVFAVNFYDWFV	YRGLGLGGSAGAGIVASEPPARVGQKVFAGNFYDWFV	30.4	17.7	15.2	1.2	0.9
A6L-4-E6-IR	YRGLVLGRISDGAGKVAFEPPARIGQKVFAGNFYDWFV	YRGILFQGRIPDGAGKVASEPPTRIGERVFAVNFYDWFV	36.1	4.2	3.6	1.1	0.9
A6L-4-H5-IR	YRGLVLGRIQDGAGKVASEPPARIGQKVFTGNFYDWFV	YRGLVLGRISDGAGKVAFEPPARIGQKVFAGNFYDWFV	28.6	24.1	22.7	1.1	0.9
A6L-4-H3-IR	YRGLVLGVSDGAGKVASDPPASIGQNVFAVNFYDWFV	YRGLVLGRIQDGAGKVASEPPARIGQKVFTGNFYDWFV	37.2	24.6	23.1	1.1	0.9
A6L-4-E5-IR	YRGLVLGRISDGAGKVAFEPPARIGQKVFAVNFYDWFV	YRGLVLGVSDGAGKVASDPPASIGQNVFAVNFYDWFV	37.1	9.1	7.2	1.3	0.8
A6L-3-C5-IR	YRGLMLDLRISDGAGKVAEQPARIGQEVYAVNFYDWFV	YRGLVLGRISDGAGKVAFEPPARIGQKVFAVNFYDWFV	42.1	30.6	24.4	1.3	0.8
A6L-4-G6-IR	YRGLDLGRISGGVGKVASESPARIGQKVYAVNFYDWFV	YRGLMLDLRISDGAGKVAEQPARIGQEVYAVNFYDWFV	42.2	21.9	17.5	1.2	0.8
A6L-3-D4-IR	YRGLVLGRISDGAGEVASEKVFAVNFYDWFV	YRGLDLGRISGGVGKVASESPARIGQKVYAVNFYDWFV	29.8	4.3	2.8	1.5	0.7
A6L-3-A7-IR	YRGLVLGRVSDGAGKVDSAPPARIGQKVFAGNFYDWFV	YRGLVLGRISDGAGEVASEKVFAVNFYDWFV	39.9	12.4	8.4	1.5	0.7
A6L-3-A6-IR	YRGLVLGRMSDGAGKVAFEPPARIGQGFAGNFYDWFV	YRGLVLGRVSDGAGKVDSAPPARIGQKVFAGNFYDWFV	31.0	21.2	14.0	1.5	0.7
A6L-4-E7-IR	YRGLVLGRISDGAGKAAEPPARIGQNVFAVNFYDWFV	YRGLVLGRMSDGAGKVAFEPPARIGQGFAGNFYDWFV	25.5	12.3	8.8	1.4	0.7
A6L-3-C6-IR	YRGLVLGRISDGAGKAAEPPARIGQKVFALNFYDWFV	YRGLVLGRISDGAGKAAEPPARIGQNVFAVNFYDWFV	38.4	12.5	7.1	1.7	0.6
A6L-4-F5-IR	YRGLVLGRISDGAGEVASEPPARIGEKVYAVNFYDWFV	YRGLVLGRISDGAGKAAEPPARIGQKVFALNFYDWFV	28.8	10.9	6.7	1.6	0.6
A6L-3-B7-IR	YRGLVLGRISDGAGKVGSEPPARSGEKVFAVNFYDWFV	YRGLVLGRISDGAGEVASEPPARIGEKVYAVNFYDWFV	33.8	6.3	4.1	1.5	0.6
A6L-4-F4-IR	YRGLVLGRISDSSGKAAEPAARISQKVFAVNFYDWFV	YRGLVLGRISDGAGKVGSEPPARSGEKVFAVNFYDWFV	27.6	9.4	5.0	1.9	0.5
A6L-4-E3-IR	YRGLVLGRISDGGKVASEPPARIGQRFVFAVNFYDWFV	YRGLVLGRISDSSGKAAEPAARISQKVFAVNFYDWFV	38.9	17.6	9.4	1.9	0.5
A6L-0-E6-IR	YRGLVLGRSSDGAGKVAFERPARIGQTVFAVNFYDWFV	YRGLVLGRISDGGKVASEPPARIGQRFVFAVNFYDWFV	38.0	6.9	3.8	1.8	0.5
A6L-0-E4-IR	YRGLVLGRISDAG#VASEPPARIGRKVFAVNFYDWFV	YRGLVLGRSSDGAGKVAFERPARIGQTVFAVNFYDWFV	31.0	31.0	1.8	17.0	0.1
A6L-0-H3-IR	YRGLVLGRISGGAGKAAEPPARIGQKVSAVNFYDWFV	YRGLVLGRISDAG#VASEPPARIGRKVFAVNFYDWFV	26.0	16.0	1.3	13.0	0.1
		YRGLVLGRISGGAGKAAEPPARIGQKVSAVNFYDWFV	27.0	26.0	2.0	13.0	0.1

Figure 1G (Con't)

Clone	Parental/Design	Sequence	Ratios over Background		Comparisons	
			E-Tag	IGFsR	IGFR/IR	IR/IGFR
A6L-4-F8-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	19	4	--	--	--
A6L-2-G9-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	26	28	--	--	--
A6L-4-E7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	39	22	--	--	--
A6L-4-G10-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	23	22	--	--	--
A6L-2-E9-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	19	22	--	--	--
A6L-2-D6-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	38	21	--	--	--
A6L-3-H12-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	34	21	--	--	--
A6L-4-A7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	24	21	--	--	--
A6L-4-B8-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	20	20	--	--	--
A6L-4-G7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	20	19	--	--	--
A6L-2-D9-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	19	19	--	--	--
A6L-4-F7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	38	18	--	--	--
A6L-4-E12-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	18	18	--	--	--
A6L-4-H7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	15	13	--	--	--
A6L-4-H12-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	14	13	--	--	--
A6L-2-A4-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	13	12	--	--	--
A6L-3-D10-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	17	4	--	--	--
A6L-2-F6-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	16	4	--	--	--
A6L-2-B11-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	15	4	--	--	--
A6L-1-B7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	26	3	--	--	--
A6L-1-D8-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	23	3	--	--	--
A6L-0-A11-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	23	3	--	--	--
A6L-3-B7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	19	3	--	--	--
A6L-1-G7-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	9	3	--	--	--
A6L-1-B9-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	20	2	--	--	--
A6L-1-C9-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	18	2	--	--	--
A6L-0-G10-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	18	2	--	--	--
A6L-1-G8-IGFR	YRGLVLGRISDAGKVASVPRIGQKVFVAVNFYDWFV	15	2	--	--	--

Figure 1H

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	GFREGNFYDWFVAQVT	--	--	--	--	--
	GFREGQRYWFWVAQVT	40.7	1.0	12.3	0.1	12.3
E4Dα-1-B8-IR	GFREGQRYWFWVAQVT	39.6	2.0	1.5	1.3	0.8
E4Dα-3-E5-IR	GFREGYFYDWFVAQVT	48.7	44.9	31.4	1.4	0.7
E4Dα-1-A1-IR	GFREGDFYEWFWVAQVT	22.9	3.3	2.4	1.4	0.7
E4Dα-2-D9-IR	GFREGQFYEWFAAQVT	41.8	38.6	26.5	1.5	0.7
E4Dα-1-B3-IR	GFREGTFYDWFVAQVT	56.3	51.2	32.6	1.6	0.6
E4Dα-1-A6-IR	GFREGNFYDWFVAQVT	48.9	42.2	26.5	1.6	0.6
E4Dα-1-A10-IR	GFREGAFYDWFVAQVT	46.9	41.5	26.2	1.6	0.6
E4Dα-1-A8-IR	GFREGAFYDWFVAQVT	44.1	31.1	19.7	1.6	0.6
E4Dα-1-B1-IR	GFREGKFYQWFEAQVT	34.0	8.1	4.8	1.7	0.6
E4Dα-2-C9-IR	GFREGDFYDWFVAQVT	45.3	40.3	22.5	1.8	0.6
E4Dα-1-A3-IR	GFREGTFYEWFWVAQVT	46.9	41.0	22.5	1.8	0.5
E4Dα-1-A9-IR	GFREGNFYDWFVAQVT	37.2	14.1	8.0	1.8	0.6
E4Dα-3-F3-IR	GFREGQFYEWFLAQVT	35.1	16.3	8.7	1.9	0.5
E4Dα-2-D3-IR	GFREGQFYDWFVAQVT	33.2	5.6	2.8	2.0	0.5
E4Dα-2-D6-IR	GFREGQFYDWFVAQVT	27.8	4.5	2.3	2.0	0.5
E4Dα-3-F10-IR	GFREGQFYDWFVAQVT	43.8	23.8	11.4	2.1	0.5
E4Dα-2-D5-IR	GFREGYFYEWFWVAQVT	25.9	7.6	3.7	2.1	0.5
E4Dα-3-F4-IR	GFREGDFYQWFEAQVT	34.6	4.0	1.9	2.1	0.5
E4Dα-3-E3-IR	GFREGSFYGFVAQVT	20.9	16.0	7.4	2.2	0.5
E4Dα-3-F8-IR	GFREGSFYGFVAQVT	43.1	11.6	5.0	2.3	0.4
E4Dα-2-C1-IR	GFREGQFYDWFVAQVT	45.3	6.6	2.9	2.3	0.4
E4Dα-1-B4-IR	GFREGIFYEWFWVAQVT					

Figure 11

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	GFREGNFYDWFVAQVT	--	--	--	--	--
E4Dα-4-H5-IR	GFREGSFYEWFOAQVT	47.2	36.0	14.7	2.4	0.4
E4Dα-1-B12-IR	GFREGNFYDWFVAAQVT	47.6	33.4	13.8	2.4	0.4
E4Dα-4-G2-IR	GFREGSFYDWFVAQVT	23.4	20.4	8.6	2.4	0.4
E4Dα-3-F9-IR	GFREGDFYDWFVAQVT	36.2	15.6	6.3	2.5	0.4
E4Dα-4-G6-IR	GFREGDFYQWFVAQVT	26.0	4.9	2.0	2.5	0.4
E4Dα-4-H9-IR	GFREGGFYDWFVAQVT	47.8	24.8	9.5	2.6	0.4
E4Dα-2-C10-IR	GFREGDFYGFVQAAQVT	42.4	23.2	9.0	2.6	0.4
E4Dα-1-B2-IR	GFREGVFYDWFVAQVT	39.4	18.7	7.2	2.6	0.4
E4Dα-3-F12-IR	GFREGGFYEWFOAQVT	38.9	16.6	5.6	3.0	0.3
E4Dα-2-D11-IR	GFREGSFYDWFVQAAQVT	40.2	11.1	3.3	3.4	0.3
E4Dα-4-H2-IR	GFREGNFYEWFOAQVT	37.8	33.9	8.2	4.1	0.2
E4Dβ-4-A12-IR	GFREGKFYDWFVLAQVT	41.1	8.3	28.7	0.3	3.5
E4Dβ-4-A10-IR	GFREGGFYEWVFAQVT	5.8	1.2	2.4	0.5	2.0
E4Dβ-4-E10-IR	GFREGRFYDWFVFAQVT	9.6	1.2	2.2	0.5	1.8
E4Dβ-4-B11-IR	GFREGTFYDWFVFAQVT	36.1	15.2	26.9	0.6	1.8
E4Dβ-4-C10-IR	GFREGGFYEWFAAAQVT	27.8	13.3	23.7	0.6	1.8
E4Dβ-4-E8-IR	GFREGDFYEWFEAAQVT	28.7	16.7	28.2	0.6	1.7
E4Dβ-4-G7-IR	GFREGHFYDWF?AQVT	30.9	14.7	24.7	0.6	1.7
E4Dβ-4-C8-IR	GFREGGFYDWFVFAQVT	35.5	22.5	32.9	0.7	1.5
E4Dβ-4-A8-IR	GFREGSFYDWFVFAQVT	31.2	14.5	22.2	0.7	1.5
E4Dβ-4-A9-IR	GFREGSFYDWFVGAQVT	35.8	9.0	13.1	0.7	1.5
E4Dβ-4-G11-IR	GFREGTFYDWFVFAQVT	28.9	9.7	13.6	0.7	1.4
E4Dβ-4-B9-IR	GFREGNFYEWFTAQVT	27.2	9.1	12.5	0.7	1.4
E4Dβ-4-F10-IR	GFREGSFYNWFVFAQVT	7.7	1.5	2.1	0.7	1.4
E4Dβ-4-D12-IR	GFREGNFYDWFVFAQVT	41.1	27.2	36.1	0.8	1.3
E4Dβ-4-B8-IR	GFREGDFYDWFVFAQVT	35.9	27.0	35.2	0.8	1.3
E4Dβ-4-G10-IR	GFREGAFYDWFVAAQVT	38.5	25.5	33.7	0.8	1.3

Figure 11 (Con't)

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E4Dβ-4-D9-IR	GFREGSFYDWFEEAQVT	34.1	19.3	25.7	0.8	1.3
E4Dβ-4-F8-IR	GFREGSFYDWFEEAQVT	39.3	35.6	44.4	0.8	1.2
E4Dβ-4-E12-IR	GFREGSFYDWFEEAQVT	40.2	27.8	33.4	0.8	1.2
E4Dβ-4-H12-IR	GFREGAFYDWFEEAQVT	41.2	27.1	32.3	0.8	1.2
E4Dβ-4-C9-IR	GFREGQFYDWFEEAQVT	38.0	22.5	27.6	0.8	1.2
E4D -4-H9-IR	GFREGNFYDWFEEAQVT	38.7	33.3	36.6	0.9	1.1
E4D -4-G9-IR	GFREGDFYDWFEEAQVT	10.9	4.9	5.6	0.9	1.1
E4Dβ-4-F12-IR	GFREGSFYDWFEEAQVT	14.8	5.9	6.1	1.0	1.0
E4Dβ-4-F9-IR	GFREGGFYDWFEEAQVT	39.3	31.3	28.3	1.1	0.9
E4Dβ-4-F7-IR	GFREGGFYDWFEEAQVT	31.0	22.2	19.5	1.1	0.9
E4Dβ-4-B7-IR	GFREGGFYDWFEEAQVT	--	--	--	--	--

Figure 11 (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
E4D-2-E7-IGFR	GFREGNFYDWFVAQVT	--	--	--	--
E4D-2-C11-IGFR	GFREGDFYDWFRAQVT	20.8	22.8	--	--
E4D-2-B1-IGFR	GFREGSFYDWFVAQVT	21.5	22.6	--	--
E4D-2-D10-IGFR	GFREGDFYDWFVAQVT	22.0	22.5	--	--
E4D-2-A9-IGFR	GFREGGFYDWFVAQVT	20.6	22.1	--	--
E4D-2-E5-IGFR	GFREGDFYDWFVAQVT	17.4	21.5	--	--
E4D-2-H9-IGFR	GFREGDFYDWFVAQVT	24.2	21.2	--	--
E4D-1B-C4-IGFR	GFREGGFYDWFVAQVT	19.1	20.7	--	--
E4D-2-E10-IGFR	GFREGDFYDWFVAQVT	24.3	20.5	--	--
E4D-2-F4-IGFR	GFREGNFYDWFVAQVT	21.0	20.5	--	--
E4D-2-C10-IGFR	GFREGNFYDWFVAQVT	25.0	20.2	--	--
E4D-3-D8-IGFR	GFREGHFYDWFVAQVT	22.8	20.1	--	--
E4D-3-F9-IGFR	GFREGQFYDWFVAQVT	21.1	19.8	--	--
E4D-1B-E5-IGFR	GFREGSFYDWFVAQVT	22.6	19.7	--	--
E4D-2-F3-IGFR	GFREGDFYDWFVAQVT	24.2	18.8	--	--
E4D-3-D5-IGFR	GFREGHFYDWFVAQVT	23.6	18.0	--	--
E4D-3-G10-IGFR	GFREGQFYDWFVAQVT	22.2	18.0	--	--
E4D-2-F6-IGFR	GFREGQFYDWFVAQVT	22.1	17.6	--	--
E4D-2-F7-IGFR	GFREGDFYDWFVAQVT	24.6	17.5	--	--
E4D-3-B7-IGFR	GFREGNFYDWFVAQVT	19.0	17.5	--	--
E4D-1B-C12-IGFR	GFREGSFYDWFVAQVT	23.0	16.4	--	--
E4D-3-B1-IGFR	GFREGHFYDWFVAQVT	23.0	16.1	--	--
E4D-2-E2-IGFR	GFREGDFYDWFVAQVT	21.6	16.0	--	--
E4D-2-D1-IGFR	GFREGHFYDWFVAQVT	21.9	14.1	--	--
E4D-1-D4-IGFR	GFREGYFYDWFVAQVT	24.5	13.2	--	--
E4D-1B-A10-IGFR	GFREGHFYDWFVAQVT	18.9	12.4	--	--
E4D-1B-A3-IGFR	GFREGDFYDWFVAQVT	23.9	10.8	--	--
E4D-1-B5-IGFR	GFREGTFYDWFVAQVT	22.2	10.8	--	--
		19.0	10.8	--	--

Figure 1J

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
D sign	GFREGNFYDWFVAQVT	--	--	--	--
E4D-1B-B8-IGFR	GFREGDYWGFEAQVT	23.8	10.7	--	--
E4D-1-G7-IGFR	GFREGDFYAWFMAQVT	14.3	10.5	--	--
E4D-1B-A11-IGFR	GFREGNFYEWFLAQVT	24.0	10.0	--	--
E4D-1-C3-IGFR	GFREGSFYDWFDAQVT	15.8	9.3	--	--
E4D-2-H1-IGFR	GFREGNFYDQFVAQVT	19.6	4.9	--	--
E4D-1-C2-IGFR	GFREGHFYEWFAAQVT	11.5	4.5	--	--
E4D-1B-A12-IGFR	GFREGNFYEWFVAQVT	18.4	3.5	--	--
E4D-1B-A1-IGFR	GFREGKFYDWFVAQVT	22.5	2.9	--	--
E4D-2-A3-IGFR	GFREGMFDVQLLAQVT	22.7	2.1	--	--

Figure 1J (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR
Design	XXXXXXXXFHENFYDWFVRQVSXXXXXX	--	--	--	--
Parental	VTFTSAVFHENFYDWFVRQVS	29.8	17.5	16.3	1.1
	TYKARFLHENFYDWFNRQVSQYFGRV	37.7	2.2	18.1	0.1
H2CA-4-F11-IR	QRLSLHEQFYDWFVGQVSPLGAGG	31.2	4.4	18.8	0.2
H2CA-4-E10-IR	GGKVNFDHEDFYGWFVQQFSGVGS DR	36.1	13.4	25.7	0.5
H2CA-4-G3-IR	LVGDAPFHEDFYDWFARQVFGCCQEQ	35.6	12.1	22.0	0.5
H2CA-3-A11-IR	TGAEVSFHENFYDWFDRQYSSWLDRD	36.0	21.1	33.5	0.6
H2CA-4-F8-IR	QPHSSRLHESFYDWFDRQVPWYALDR	37.1	23.3	34.3	0.7
H2CA-4-G4-IR	SRALAAVHEQFYDWFVRQVSGLDWGY	39.8	25.0	35.6	0.7
H2CA-4-F4-IR	QPKDGTLHENFYDWFVRQVSSSGWVG	33.5	5.1	6.6	0.8
H2CA-4-H10-IR	RGRLIQLHEDFYDWFRLRQVSGMGGS	36.1	19.6	25.1	0.8
H2CA-4-F1-IR	QRGAPKSDENFYDWFVRQVLRFGEND	39.3	24.3	31.9	0.8
H2CA-3-D5-IR	AARTSLFHEDFYEWFDQRVRQEGMWG	8.2	2.6	3.2	0.8
H2CA-4-E11-IR	GTSNHS LHENFYDWFVRQLSSVQSSG	35.9	9.9	12.1	0.8
H2CA-3-B6-IR	VSHVHLFHENFYDWFVRQLAAEGFSG	37.3	30.1	36.2	0.8
H2CA-3-A9-IR	GRQDSGLHEHFYDWF SRQVQGEVALG	38.6	35.4	37.3	1.0
H2CA-4-H5-IR	SNDERQFHETFYDWFVRQVSADGADR	29.3	5.1	5.6	0.9
H2CA-3-C9-IR	LSTEQR FHEKFYDWFVHVQVSTSGGT	37.2	16.9	19.1	0.9
H2CA-3-A10-IR	SLSRQEHFENFYDWFARQVSELEGVV	29.2	28.6	32.2	0.9
H2CA-3-A3-IR	IPGRRSLHENFYDWFVRQVSPGGGSA	32.4	29.1	31.6	0.9
H2CA-4-G8-IR	TQKAQSLDEKFYDWFVRQVSGGLTG	36.1	34.4	36.4	0.9
H2CA-4-G9-IR	VSQLSDFHENFYGWFARQIAGQAEWT	34.2	35.5	37.7	0.9
H2CA-4-G10-IR	NGTSQALHQNFYDWFQAQISGSEPGP	37.0	36.0	40.0	0.9
H2CA-4-H7-IR	VGQSVTFHGDFYDWFDRQLSGSQEFG	37.5	36.7	39.5	0.9
H2CA-4-F9-IR	TIDHHP LHEQFYDWFARQVSDLES LG	37.7	37.6	39.9	0.9
H2CA-4-F7-IR	PNVGYAFHENFYDWFTRQVSIIEKAG	18.7	3.6	3.5	1.0
H2CA-3-D10-IR	SRGSGVFHESFYNWFDRQVSEW IQFG	26.5	21.4	21.5	1.0
H2CA-3-B1-IR	QPVSGSVHERFYDWFVRQVSGSAGGG	32.9	22.9	22.4	1.0
H2CA-3-A5-IR	ASQLPPVYENFYEWFDQRVSLDAQRE	26.6	27.7	28.5	1.0
H2CA-4-F10-IR					

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CA-3-D9-IR	VSGRGAFHENFYDWFVRQVFRDEQDT	36.6	30.6	30.9	1.0	1.0
H2CA-3-C2-IR	ARPPPTVHENFYDWFVRQVSETWRQD	38.3	30.7	31.0	1.0	1.0
H2CA-4-C1-IR	QGGDRLFHERFYDWFDRLVSSDSTGE	34.1	30.7	30.4	1.0	1.0
H2CA-4-E2-IR	QHIAAGLHENFYDWFIRQVSGVNVPA	33.9	31.0	31.8	1.0	1.0
H2CA-4-H9-IR	QPNDDLHENFYDWFVRQVSNVAVDGG	38.9	31.1	31.4	1.0	1.0
H2CA-3-D2-IR	PVEFTVYHDNFYDWFARQVSDGLGQF	33.0	31.1	29.8	1.0	1.0
H2CA-3-B3-IR	FCVQASIHENFYDWFVRQVAENQVFS	35.3	31.4	30.0	1.0	1.0
H2CA-4-G11-IR	GRPRGSFHENFYDWFARQVSGDGAGT	37.9	31.9	31.0	1.0	1.0
H2CA-4-F2-IR	IVGASLCHESFYDWFACQVTNLQSQG	38.1	32.0	31.9	1.0	1.0
H2CA-3-C5-IR	IGLRQMFHENFYDWFAREVSKAEGDG	36.9	32.3	31.6	1.0	1.0
H2CA-3-B2-IR	LGAIEGHGNFYDWFVRQVSLDVGE	36.6	32.7	32.5	1.0	1.0
H2CA-3-B11-IR	LNALQQLHENFYDWFGRQVSATPPGG	35.5	32.8	33.3	1.0	1.0
H2CA-4-G2-IR	VGNCDTFPENFYDWFACQVSELGGMN	35.9	33.0	33.4	1.0	1.0
H2CA-3-A4-IR	FSQDGNFHENFYDWFDRQLSLVGAGT	33.3	33.0	32.9	1.0	1.0
H2CA-4-H3-IR	PAGNRALHESFYDWFVRQVSEFQLGA	39.5	33.7	33.7	1.0	1.0
H2CA-4-G5-IR	DRLRARFNENFYDWFDRQVSGQSNP	35.3	34.0	35.6	1.0	1.0
H2CA-4-E8-IR	VLGVAQFHDKFYDWFARQVSLQESAG	35.7	34.7	34.9	1.0	1.0
H2CA-4-G6-IR	GVVGGAFHEQFYDWFDRQVSAAFKGD	36.2	35.0	33.5	1.0	1.0
H2CA-3-B7-IR	DESEMRLEQFYDWFARLVSLGSGA	37.6	36.5	35.3	1.0	1.0
H2CA-3-B4-IR	EGGGVAIHENFYDWFDRQVSLQWSD	39.8	36.5	35.1	1.0	1.0
H2CA-3-C7-IR	SRIVSRFHENFYDWFVRQVSGDAPVQ	40.2	36.7	35.9	1.0	1.0
H2CA-4-E5-IR	IPAGAQLHENFYDWFARQVSGEDGGA	37.3	37.0	36.3	1.0	1.0
H2CA-4-E7-IR	GSSAAGFDEQFYDWFDRQVSEAFRDG	39.7	37.6	37.6	1.0	1.0
H2CA-3-B9-IR	RLALRTFHFQDFYDWFVRQVAAEDTDP	39.4	37.7	37.6	1.0	1.0
H2CA-4-F5-IR	QGSFAVLHENFYDWFARQVSGVEGLA	38.8	38.0	37.8	1.0	1.0
H2CA-3-B10-IR	QGNMSALHENFYDWFVRQVSEADRV	41.9	38.9	38.0	1.0	1.0
H2CA-3-A12-IR	VAYPALLHEQFYDWFVRQVSAVAGTT	37.8	7.3	6.3	1.2	0.9
H2CA-3-A8-IR	PDTINSQHKNFYDWFVRQVSGVGTSS	36.8	22.5	19.2	1.2	0.9

Figure 1K (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFSR	IR	IGFSR	IR	IR/IGFSR
H2CA-3-D12-IR	XXXXXXXXXPHENFYDMFVRQVSGXXXXXX	36.8	34.1	29.6	1.2	0.9	
H2CA-3-B5-IR	SEDVDSRHNFYDMFVRQVSGIGLQD	38.8	35.2	30.5	1.2	0.9	
H2CA-4-E1-IR	PAPADAFDHNFYDMFARQLSATTIQ	29.8	12.5	11.3	1.1	0.9	
H2CA-3-D3-IR	WVQRISIHENFYDMFVRQISGSAPP	33.1	29.9	27.5	1.1	0.9	
H2CA-4-E3-IR	GNVRQGFHQFYDMFARQVSGSEGDA	33.3	32.3	30.2	1.1	0.9	
H2CA-4-E12-IR	PDAEKQFHETFYGMFVRQISSEDSANS	36.0	32.4	29.4	1.1	0.9	
H2CA-3-A6-IR	FRGVHCDENFYDMFVRQVSGGALLEG	34.0	33.1	30.6	1.1	0.9	
H2CA-4-E9-IR	ETPLTELHEQFYDMFVRQVSGFPGGV	38.8	33.7	29.7	1.1	0.9	
H2CA-4-F3-IR	QHRGPHFHEFYDMFVRQVSSAVPSD	41.0	34.2	32.0	1.1	0.9	
H2CA-4-H6-IR	RQDPGLFDHNFYDMFDRLVSAWDGQE	37.1	34.5	30.8	1.1	0.9	
H2CA-4-H2-IR	QAAVGVCKDFYAMFACQVREDFAKA	41.8	35.3	32.8	1.1	0.9	
H2CA-3-D4-IR	RNNWLQFNENFYDMFDRQVSRMLLGG	38.7	35.5	32.3	1.1	0.9	
H2CA-3-D1-IR	RSEQYRFHENFYEMFDRQVSRMGLLG	34.5	35.5	31.3	1.1	0.9	
H2CA-3-C1-IR	GAGGRDFEDFYDMFVRQVSGQVTSG	39.9	36.1	32.9	1.1	0.9	
H2CA-3-D8-IR	SPEGNLVHDQFYDMFVRQJSSTAGT	37.8	36.7	33.1	1.1	0.9	
H2CA-4-H4-IR	QGGGLDFDEDFYDMFARQVSRDRAD	38.5	37.0	33.7	1.1	0.9	
H2CA-4-F6-IR	LSQGVGFQENFYEMFVRQVSGWDGRD	38.7	37.5	35.2	1.1	0.9	
H2CA-4-E4-IR	VFERSRCHDNFYDMFARQVSGTQPPG	38.6	38.0	34.7	1.1	0.9	
H2CA-3-C11-IR	LLASRAFHENFYDMFARQVSGTQPPG	40.3	38.3	36.1	1.1	0.9	
H2CA-3-C4-IR	VPDAQIFHESFYDMFVRQASAGGPAD	41.9	38.4	35.0	1.1	0.9	
H2CA-4-E6-IR	ANQMGRFHDNFYDMFDRQVSRYERGT	39.3	38.8	35.8	1.1	0.9	
H2CA-3-A7-IR	PSRKDGLHQSYDMFARQVQDMEGRA	42.5	39.2	35.5	1.1	0.9	
H2CA-4-G12-IR	QAVTRRFHENFYDMFARQVSEGGWS	35.3	15.2	11.6	1.3	0.8	
H2CA-3-D6-IR	GVAVGQYQANFYDMFVRQVDMGNSGG	37.6	19.4	15.1	1.3	0.8	
H2CA-4-H12-IR	GHQDRLLESFYDMFVRQVSEAECCG	39.4	36.2	27.6	1.3	0.8	
H2CA-3-D11-IR	DRPSSFIFHENFYEMFARQVSGSGSSG	40.0	38.4	29.3	1.3	0.8	
H2CA-3-C12-IR	ERTAEITLHEQFYDMFVRQVSMADGES	38.1	32.9	27.2	1.2	0.8	
	LTSQLLSHEDFYDMFVRQVSGVGGSG	38.5	38.4	31.7	1.2	0.8	
	PDRSRDLDDNFYDMFVRQVSGVQINED						

Figure 1K (Con't)

Figure 1K (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXHNFYDWFVRQVSXXXXXX	--	--	--	--	--
H2CA-4-G7-IR	RAGGVGLHDNFDYDWFVRQVSGGDSGP	35.9	34.7	23.7	1.5	0.7
H2CA-3-C6-IR	ADCYVQLHNFYDWFVRQVCNLOEGM	38.7	37.6	28.2	1.3	0.7
H2CA-3-B8-IR	ROGHAGFHDNFDYDWFVRQVSGSTPQV	37.8	19.6	9.9	2.0	0.5

Figure 1K (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXHNFYDFVFRQVXXXXXX	--	--	--	--	--
H2CA-4-G9-IGFR	VTFTSAVFHENFYDFVFRQV	29.8	17.5	16.3	1.1	0.9
H2CA-4-H6-IGFR	GIISQSCPEFYDFWFGVSDPWMCW	8.6	9.5	0.6	16.0	0.1
H2CA-4-F-IGFR5	VGRASGFPEFYDFWFGRLSLQSGEQ	4.9	10.5	0.7	14.6	0.1
H2CA-4-H8-IGFR	VGYQGGDENFYDFIRQVSGRLGVQ	5.5	9.7	0.8	12.3	0.1
H2CA-4-F11-IGFR	SACQFDCHEFYDFWFGVSGGAAYG	5.6	9.2	1.0	9.4	0.1
H2CA-4-F6-IGFR	SAAQLFFQESFYDFWFLRQVAESSQPN	3.5	6.8	1.0	6.7	0.1
H2CA-4-F10-IGFR	AVRATRFEAFYDFWFRQISDGQGNK	3.9	7.3	1.1	6.4	0.2
H2CA-1-A3-IGFR	VNQSGSIHENFYDFWFERQVSHQGVNR	4.9	5.7	1.0	5.9	0.2
H2CA-3-C8-IGFR	APDPSDFQEIFYDFWFRQVSRMPGGG	7.7	3.8	0.8	5.1	0.2
H2CA-2-B9-IGFR	SSCDGAGHESFYEWFRQVSLSLKKG	15.1	5.6	1.2	4.8	0.2
H2CA-4-H4-IGFR	RAGSSDFHEDFYEWFRQVSTGVGGG	9.3	7.0	1.7	4.2	0.2
H2CA-4-F7-IGFR	QAVQPGFHEFYDFWFRQVSTGVGGG	3.9	4.1	1.0	4.2	0.2
H2CA-3-D6-IGFR	SSIIGGFHENFYDFWFSRQLSQSPPLK	1.5	3.2	0.8	4.1	0.2
H2CA-3-D8-IGFR	QSPVSSHEDFYDFWFRQVSAQGAHQ	8.3	9.0	2.2	4.0	0.3
H2CA-4-G11-IGFR	NYRRQVFNENFYDFWFRQVSLVTPG	10.9	7.2	1.8	4.0	0.3
H2CA-4-F1-IGFR	TLDGGSFEEFYDFWFRQVSLYRTNPD	10.8	9.5	2.5	3.9	0.3
H2CA-3-D7-IGFR	FYVQQWGHENFYDFWFRQVSGGAG	5.8	3.5	0.9	3.8	0.3
H2CA-1-A7-IGFR	LRRQAPVEENFYDFWFRQVSGDRVGG	13.3	3.0	0.8	3.7	0.3
H2CA-2-B4-IGFR	RCGRELYHSTFYDFWFRQVAGRTCPS	8.0	2.2	0.6	3.7	0.3
H2CA-2-B3-IGFR	CCLLCRFQQNFYDFWFCQGISRLRPL	3.5	4.1	1.1	3.6	0.3
H2CA-2-B2-IGFR	PPLASDLVQFYGFVQVQVSPPPGRGG	7.7	3.8	1.0	3.6	0.3
H2CA-3-D4-IGFR	GAPVDQLHEDFYDFWFRQVQAATG	4.1	3.4	1.0	3.5	0.3
H2CA-4-F2-IGFR	RSASGSLPEQFYDFWFRQVSLSGTDK	17.6	13.8	4.1	3.4	0.3
H2CA-3-D11-IGFR	SRVTTVFHENFYDFWFRQVSDSAISG	9.3	12.8	4.2	3.0	0.3
H2CA-4-H9-IGFR	DERGGKFRDFYDFWFRQVSESFRGQ	12.2	6.9	2.3	3.0	0.3
H2CA-2-B11-IGFR	RGAVAGFHDQFYDFWFRQVSRVHKFG	8.7	5.6	1.9	3.0	0.3
H2CA-3-E8-IGFR	AICDAGFHEFYDFWFRQVSDCGRQS	11.9	4.6	1.6	3.0	0.3
	LGYQEPFQQNFYDFWFRQVSGAENAG	13.2	6.3	2.2	2.9	0.3

Figure 1L

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CA-3-E6-IGFR	XXXXXXFHENFYDWFVRQVXXXXXXXX	--	--	--	--	--
H2CA-4-F4-IGFR	WRGHGTFHEDFYDWFVRQVSGSGSST	15.7	8.7	3.1	2.8	0.4
H2CA-3-D10-IGFR	GGRVGVLHENFYDWFDRQVSLRGADG	11.5	7.4	3.0	2.5	0.4
H2CA-3-E1-IGFR	CNLTAGFHEQFYHWFATQVCGDAENA	9.4	6.8	2.9	2.3	0.4
H2CA-2-B6-IGFR	ERGEDMFHENFYDWFVRQISGRQGGG	12.5	6.4	2.8	2.3	0.4
H2CA-3-E11-IGFR	TNQGVSFYDSFYGWFVRQIQYGVDSG	18.0	6.2	2.7	2.3	0.4
H2CA-4-H2-IGFR	HLADGQFHEKFYDWFVRQISSRCNDC	4.7	2.2	1.0	2.2	0.5
H2CA-3-C11-IGFR	QTFGKSLHENFYDWFVRQVSREEGGD	9.8	9.9	4.8	2.1	0.5
H2CA-2-B8-IGFR	FRTLAAQHDSFYDWFDRQVSGAAGER	9.3	3.3	1.6	2.1	0.5
	SASTHQFHENFYDWFVRQVSGAQKIL	14.6	7.9	3.9	2.0	0.5

Figure 1L (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXFXHXXFYXWFXXXXXX	--	--	--	--	--
H2CBα-3-D11-IR	GPRQRLHDAFYSWFDALRVN	27.8	13.0	24.8	0.5	1.9
H2CBα-3-H12-IR	LGT LAVFHEL FYGWFERQLGG	27.4	7.2	12.4	0.6	1.7
H2CBα-3-A10-IR	LGGYCGFNCFYRWF ^Q DNLADR	27.1	13.2	22.3	0.6	1.7
H2CBα-3-A5-IR	FSGWADYQSGFYQWFAEELAN	28.3	16.1	28.1	0.6	1.7
H2CBα-3-C4-IR	WGPFSVFDES FYRWFAQASDD	30.7	17.2	29.2	0.6	1.7
H2CBα-3-B8-IR	PRNEGLVHGLFYDW ^F Q ^R ALSG	25.6	11.3	18.6	0.6	1.6
H2CBα-3-H11-IR	DEGGAPLDVMFYRWF ^E QAVRG	28.8	14.0	22.4	0.6	1.6
H2CBα-3-E10-IR	QSGNRGSHGAFYSWFRDVLAN	27.7	14.3	23.0	0.6	1.6
H2CBα-3-C2-IR	MRQRDGFNSFYGWFAAALGE	28.4	17.0	26.7	0.6	1.6
H2CBα-3-F6-IR	SEERKKVHSQFYSWFDRQLLG	27.3	14.5	21.8	0.7	1.5
H2CBα-3-D4-IR	PSPNAPFHGGFYDWFDWVQGS	29.0	18.9	27.1	0.7	1.4
H2CBα-3-A7-IR	FHRPGSFNTNFYQWFD ^D QMNQ	29.1	19.4	26.9	0.7	1.4
H2CBα-3-H4-IR	SDDSS ^T LNGRFYTW ^F HMQLLD	27.2	20.1	27.9	0.7	1.4
H2CBα-3-B7-IR	QRGGGFHEGFYSWFRSQSLL	28.6	18.0	23.6	0.8	1.3
H2CBα-3-F9-IR	SGSRPVFHEQFYEW ^F VDQLGL	26.1	19.1	24.3	0.8	1.3
H2CBα-3-H6-IR	GGSSQAFHGAFYEW ^F SAQLRG	24.8	21.6	27.3	0.8	1.3
H2CBα-3-F5-IR	AFVSE ^R VNQRFYDWFRDQ ^R MS	29.4	22.0	27.8	0.8	1.3
H2CBα-3-A2-IR	VRHPT ^R PHDEFYRW ^F TEQLTT	30.7	22.5	29.1	0.8	1.3
H2CBα-3-F3-IR	ARLLNIFDRGFYNW ^F Q ^R QLDE	16.3	6.7	9.0	0.7	1.3
H2CBα-3-G6-IR	PSLSSNLHESFYRW ^F DQ ^L VST	24.9	21.0	24.4	0.9	1.2
H2CBα-3-G7-IR	FAFGLGFHQGFYDWFAHQ ^L EG	24.4	18.7	23.0	0.8	1.2
H2CBα-3-C5-IR	VSATVMLHREFYDW ^F GLQLLD	26.4	21.2	25.4	0.8	1.2
H2CBα-3-G1-IR	GGVSGVLH ^D RFYSW ^F ERQ ^L AG	26.9	21.5	26.3	0.8	1.2
H2CBα-3-E3-IR	GLGIASFHEGFYSW ^F TAQLGA	24.2	17.2	19.3	0.9	1.1

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFsR/IR IR/IGFsR
H2CB α -3-A9-IR	XXXXXXFHXXFYXWFXXXXXX	30.5	21.7	24.1	0.9 1.1
H2CB α -3-C11-IR	RVDAALNAGFYEWFRGVIQG	26.4	21.8	23.2	0.9 1.1
H2CB α -3-B4-IR	GGAGRSFHDAFYEWFERQMAG	30.9	22.0	24.3	0.9 1.1
H2CB α -3-F11-IR	EGARQGFHARFYSWFAQQLAL	24.5	22.5	23.9	0.9 1.1
H2CB α -3-G10-IR	VLLPGVVHGGFYDWFSRQLSS	28.3	23.6	27.1	0.9 1.1
H2CB α -3-D7-IR	GALSDRYNNVFDWFRQLLG	31.4	23.6	25.3	0.9 1.1
H2CB α -3-E2-IR	PDSFMSLHQRFYSWFOAQVGT	26.8	24.0	25.7	0.9 1.1
H2CB α -3-B5-IR	RVYKANFHNEFYGWFRQLLG	28.7	25.0	26.4	0.9 1.1
H2CB α -3-C7-IR	HSGMRDVHARFYSWFSEQLSG	30.0	25.2	28.7	0.9 1.1
H2CB α -3-G9-IR	ARLLERFQDPFYEWFEETLMGD	27.8	25.2	26.7	0.9 1.1
H2CB α -3-A12-IR	RNSSGNFHDKFYNWFEAQLKG	28.0	26.4	28.7	0.9 1.1
H2CB α -3-C9-IR	GSMSPVNDQFYGWFRDLVDE	32.1	28.7	31.9	0.9 1.1
H2CB α -3-B10-IR	SCTGRQFDGCFYAWFEDQLVG	33.5	30.8	33.2	0.9 1.1
H2CB α -3-E1-IR	GIAVQSLHDSFYRWFDNALGS	31.7	30.5	29.0	1.1 1.0
H2CB α -3-G12-IR	IGPPGSLHRGFYDWFAEQVEA	29.1	31.4	29.8	1.1 1.0
H2CB α -3-F7-IR	GAAGISFHRGFYDWFAAQVRD	23.2	20.7	20.3	1.0 1.0
H2CB α -3-G8-IR	GVDVTDFHKDFYSWFQRQLNG	22.8	20.9	20.4	1.0 1.0
H2CB α -3-C6-IR	WAGRAGIHGGFYEWFNRLRG	26.7	21.2	22.0	1.0 1.0
H2CB α -3-H9-IR	LGQLAAFLHGFYEWFSVAVA	23.4	22.5	22.0	1.0 1.0
H2CB α -3-H8-IR	VHSVSRNLNVGYQWFQDQLSG	23.5	23.4	23.2	1.0 1.0
H2CB α -3-F2-IR	LGLMAIFDRGFYGWFEQQLSG	25.5	24.3	25.2	1.0 1.0
H2CB α -3-D5-IR	VARGSSLHDDFYEWFSQQLRT	26.7	24.5	25.6	1.0 1.0
H2CB α -3-D10-IR	LGYIGALNTQFYSWFADLVGS	26.8	24.9	24.9	1.0 1.0
H2CB α -3-F10-IR	EDSRLRLHEGFYGWFRKQLGD	25.7	25.6	26.1	1.0 1.0
	GRDNMKFHSGFYDWFQTQLAG				

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CBα-3-D6-IR	XXXXXXXXHXXFYXWFXXXXX	--	--	--	--	--
H2CBα-3-H3-IR	AGVMGGFHQEFYLWFERALSN	27.9	26.0	25.8	1.0	1.0
H2CBα-3-F4-IR	AGHVGVYDGFYGFWEQLGA	27.0	26.9	26.2	1.0	1.0
H2CBα-3-E9-IR	FVQNIQFDYDFYGFWEVEK	31.2	27.2	27.7	1.0	1.0
H2CBα-3-H10-IR	PVGIGGLHRAFYQWFQSDA	31.6	27.7	28.2	1.0	1.0
H2CBα-3-G2-IR	GSREQADHQAFYDWFNLVLGV	26.9	27.9	28.8	1.0	1.0
H2CBα-3-B2-IR	AGGRKPFHDDFYGWFRLQAE	29.1	28.1	28.8	1.0	1.0
H2CBα-3-E8-IR	DLASHGFHDAFYNWFVSQNS	29.4	28.1	28.2	1.0	1.0
H2CBα-3-E5-IR	GSNGGVHGFYAFWFEALSG	31.5	28.4	29.1	1.0	1.0
H2CBα-3-E6-IR	RGRASTFHDGFYGFWSQQLRF	33.0	28.7	28.9	1.0	1.0
H2CBα-3-E7-IR	SPARRVSHHDFYGFWFAKQLES	29.6	29.0	28.1	1.0	1.0
H2CBα-3-C8-IR	SSDVGAFHSAFYDWFKAQLSG	30.4	30.2	30.2	1.0	1.0
H2CBα-3-A4-IR	PTVHRAFDLDFYGFWFAKQVED	31.9	31.2	31.5	1.0	1.0
H2CBα-3-D1-IR	SSNTVGLDERFYAFWVDQLGA	32.2	31.9	32.6	1.0	1.0
H2CBα-3-B9-IR	PGAAEGFHSFYDWFQAQVSG	32.9	32.5	31.5	1.0	1.0
H2CBα-3-D8-IR	MRSEASFHVEFYSWFEQLRS	33.2	33.8	33.3	1.0	1.0
H2CBα-3-F1-IR	VSRYGQDGFYHWFSDLLKG	26.3	20.2	19.1	1.1	0.9
H2CBα-3-A11-IR	RPSSGGLHYGFYHWFVRVQEE	28.8	28.0	26.4	1.1	0.9
H2CBα-3-A3-IR	SNIEEHFMQFYRWFSQDQGN	20.5	21.5	17.7	1.2	0.8
	ANDCLGLHAGFYGFACQLGG	30.4	29.6	21.8	1.4	0.7

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CB β -3-E8-IR	XXXXXXFHXXFYXWFXXXXXX	15.9	1.9	11.8	0.2	6.1
H2CB β -4-F8-IR	TGHRGLDEQFYWFRDALSG	13.4	0.8	2.6	0.3	3.4
H2CB β -3-C4-IR	VLTSNTLHQRFYSWFAAARRE	21.1	1.3	4.0	0.3	3.1
H2CB β -3-D5-IR	CVAQGGFQSSFYCWFAGLDID	14.0	3.3	10.2	0.3	3.1
H2CB β -3-E6-IR	NGQSSRFHTAFYDWFAAQLSG	5.7	0.7	2.1	0.3	3.1
H2CB β -4-G12-IR	SVPRGTVHDAFYQWFREVALG	6.8	1.8	5.4	0.3	3.1
H2CB β -4-F4-IR	GARGSTFHDQFYEWFWVQLGD	17.9	1.9	5.6	0.3	3.0
H2CB β -4-F11-IR	PPGMNGFHTSFYSWFDQLGD	15.0	1.7	4.8	0.3	2.9
H2CB β -3-E5-IR	AVGTLGYHSGFYRWFERQLGG	17.0	1.8	5.0	0.4	2.8
H2CB β -4-F2-IR	ELQARGVHRNFYRWFEAQVSG	15.9	1.3	3.4	0.4	2.6
H2CB β -4-G4-IR	HRVARAFHEQFYDWFEKAVSG	8.7	1.4	3.5	0.4	2.6
H2CB β -3-C8-IR	GAMEPDYHRSFYQWFAAAALGE	4.9	1.4	3.2	0.4	2.3
H2CB β -4-F10-IR	CPDRQSVDDRFYNWFADALAS	10.2	1.0	2.4	0.4	2.3
H2CB β -4-H4-IR	GGAQISFHERFYQWFLQEAAG	20.8	4.2	9.5	0.4	2.3
H2CB β -4-G6-IR	HKRGIVQHGAFYAWFDSLSSG	14.5	5.6	8.5	0.7	1.5
H2CB β -4-H1-IR	QASDNRS \overline{D} GQFYLWF \overline{E} KLLSS	17.0	10.1	13.2	0.8	1.3
	DRGRMGVDEGFYNWFARQ \overline{M} QE					

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXXXFYXWFXXXXX	--	--	--	--	--
H2CB-3-D2-IGFR	VTFTSAVFHENFYDWFVRQVS	29.8	17.5	16.3	1.1	0.9
H2CB-3-C12-IGFR	TASQECFDDGFYGFRAWRCT	22.9	18.6	11.8	1.6	0.6
H2CB-3-B11-IGFR	SLDWRWSEEPFYRWFQRALAG	17.3	19.6	13.0	1.5	0.7
H2CB-4-E2-IGFR	CMSLSDCHRKIFYGWFKSQGGE	24.6	17.1	11.9	1.4	0.7
H2CB-3-A5-IGFR	LALCRRSPGSFYGFQAAVGC	22.4	21.0	16.5	1.3	0.8
H2CB-4-G12-IGFR	PRSATMSDGGFYWWFASQLGL	28.8	26.1	22.6	1.2	0.9
H2CB-3-B2-IGFR	LRRSSVFHDPFYE*ISRLVGG	23.7	23.8	19.4	1.2	0.8
H2CB-3-D1-IGFR	ARLQQQFHGGFYEWFRAQVSP	23.0	19.9	16.4	1.2	0.8
H2CB-3-B6-IGFR	AQLDNLCHEPFYSWFCVATRE	21.5	19.5	15.7	1.2	0.8
H2CB-4-F7-IGFR	WTCDTAFHQDFYQWFCDKLGV	16.3	4.5	3.7	1.2	0.8
H2CB-4-G8-IGFR	GKEGFLDRDFYWWFREQLGP	22.0	19.0	18.0	1.1	0.9
H2CB-3-D4-IGFR	GRAPSSFDCCDFYCWFRNQVS	20.2	18.6	16.5	1.1	0.9
H2CB-3-D5-IGFR	DVEAETQHRLFYAWFLSQLGS	21.9	18.3	16.9	1.1	0.9
H2CB-4-E6-IGFR	ISVTAVFHGDFYGFWNEQVSK	21.4	17.9	16.4	1.1	0.9
H2CB-3-C2-IGFR	NSEHGRLDVDFYGFWARVIQQ	19.6	15.8	14.8	1.1	0.9
H2CB-3-A6-IGFR	GPLGDGCQDGFYGFWMCQVST	18.8	12.2	10.8	1.1	0.9
H2CB-4-H12-IGFR	KRSAYNFHDPFYDWMFRMLSG	26.8	29.0	28.1	1.0	1.0
H2CB-3-B10-IGFR	ASEPGGYLDPFYGFWFRQLRA	23.9	28.3	28.1	1.0	1.0
H2CB-4-F11-IGFR	NRDGGVHSGFYFNWFRLLQSLG	27.1	27.5	27.3	1.0	1.0
H2CB-4-G11-IGFR	ASKGSSLHNDFYGFWFAQLLAR	25.5	25.5	24.6	1.0	1.0
H2CB-4-E12-IGFR	ANVSMWIVGVFYDWFDAQLRQ	25.3	25.4	25.3	1.0	1.0
H2CB-4-G10-IGFR	RTSPGSLHDPFYDWFQQQLGG	27.8	24.9	24.7	1.0	1.0
H2CB-3-B9-IGFR	PGVMSSFHGGFYSWFREQLNG	25.1	24.6	24.2	1.0	1.0
H2CB-3-B7-IGFR	CLANSEHDHSFYGFWFCQALGG	25.6	23.3	23.7	1.0	1.0
H2CB-4-H4-IGFR	GGSMGMHGSFYEWFAQLRS	24.0	23.2	23.5	1.0	1.0
	RPQGGSIHAGFYQWFRDAVAG	23.5	23.1	23.8	1.0	1.0

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Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D sign	XXXXXXXXFHX ^{XX} FYXWFXXXXXXXX	--	--	--	--	--
H2CB-4-H10-IGFR	GALSSLFDAAFYDWFNRLQLEG	21.9	22.4	23.3	1.0	1.0
H2CB-4-H5-IGFR	KVDLRGFHDGFYGF ^W FA ^R QLAG	22.3	22.3	21.6	1.0	1.0
H2CB-4-G7-IGFR	CSGLQRCHDSFYSWFESVVRE	23.1	21.6	20.6	1.0	1.0
H2CB-4-F4-IGFR	DSLGISFHEGFYDWFRRLQ ^L DM	21.3	20.9	21.3	1.0	1.0
H2CB-3-D8-IGFR	SGVFNGTFYDWFR ^I QLGE	20.0	20.5	21.6	1.0	1.0
H2CB-4-E4-IGFR	GYREMRSDLGFYQWFRDQLGL	21.6	20.5	21.2	1.0	1.0
H2CB-4-E5-IGFR	SVFMQH ^D HVGFYAWFRSL ^M EE	22.0	19.9	20.9	1.0	1.0
H2CB-4-E8-IGFR	FRHIT ^E VD ^R SFYGW ^F VEQLRG	21.1	19.7	20.7	1.0	1.1
H2CB-3-D12-IGFR	WAGGSDVDGSFYDW ^F QRL ^L AS	26.6	17.3	16.8	1.0	1.0
H2CB-4-G9-IGFR	GLQNVSFHSGFYEW ^F ARQ ^V SQ	21.6	14.5	15.2	1.0	1.1
H2CB-3-C8-IGFR	SRVSDPYHVGFYQ ^W FEEVVRG	20.8	13.4	13.9	1.0	1.0
H2CB-3-A12-IGFR	MGGATFFHTGFYDW ^F AAQLQH	28.6	27.5	29.2	0.9	1.1
H2CB-3-B12-IGFR	RPASRPFHSGFYQW ^F ADQLSH	27.8	25.2	27.1	0.9	1.1
H2CB-3-A9-IGFR	GLAPGNFHEDFYRW ^F QEQT ^L G	27.7	24.3	25.7	0.9	1.1
H2CB-3-A3-IGFR	TAAISDFNSLFYGW ^F EQ ^L LSS	26.9	24.1	26.5	0.9	1.1
H2CB-3-B4-IGFR	LDEDLPQHAGFYGW ^F AEALGV	25.8	23.8	25.3	0.9	1.1
H2CB-4-E7-IGFR	ASHKSAFDDNFYRW ^F SMQLRD	24.6	21.6	24.0	0.9	1.1
H2CB-4-G6-IGFR	HTGAGDLHGAFYNW ^F LEQLGG	22.4	21.1	23.0	0.9	1.1
H2CB-4-E9-IGFR	RRGRDGFHGGFYDW ^F AAQLSD	24.3	20.7	22.0	0.9	1.1
H2CB-4-H2-IGFR	GNFREAFHADFYSW ^F ERQLQS	21.6	20.2	21.9	0.9	1.1
H2CB-3-A10-IGFR	RDTLPAPHQH ^F YQW ^F EKQVSA	24.3	19.9	21.5	0.9	1.1
H2CB-3-C4-IGFR	ERETA ^F FGQAFYQWFRDQ ^I AG	23.1	19.2	22.0	0.9	1.1
H2CB-3-B5-IGFR	WGE ^G GGFYDW ^F YDQLGW ^E PSH	24.2	18.8	20.7	0.9	1.1
H2CB-4-G4-IGFR	SLVAA ^D LHEGFYGW ^F RSQLGG	21.7	18.7	21.2	0.9	1.1
H2CB-3-D9-IGFR	TSEVGD ^F HA ^F YSW ^F EIQLGR	24.4	18.6	20.0	0.9	1.1
H2CB-3-C3-IGFR	TGADGLLHARFYAW ^F E ^E QLRE	20.3	18.4	21.1	0.9	1.1
H2CB-3-D3-IGFR	RRSDSSLHRSFYDW ^F SVQLLN	22.5	18.3	21.3	0.9	1.2
H2CB-4-F2-IGFR	SESKYLLHSGFYGW ^F EAQLRG	18.0	16.8	18.3	0.9	1.1

Figure 1N (Con't)

Clone	Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		XXXXXXXXFHXFXFXWXXXXXXXX	--	--	--	--	--
H2CB-4-H1-IGFR		HGVIRADHTGFYGFWSKQLSD	18.3	15.3	16.5	0.9	1.1
H2CB-4-F9-IGFR		LINA.VFRRGFYAWFEEQVSK	22.9	14.4	15.3	0.9	1.1
H2CB-4-E10-IGFR		LQRYIGFHDPPYDWFSLSG	26.1	20.1	24.5	0.8	1.2
H2CB-4-F8-IGFR		MRTAELFHVGFDWFDALMD	21.5	14.8	19.0	0.8	1.3
H2CB-3-A8-IGFR		WAPPDALHGQFYRWFORQLDQ	20.7	14.7	18.2	0.8	1.2
H2CB-4-F1-IGFR		AVHAATFHDDFYRWFEQVGS	22.2	14.6	18.8	0.8	1.3
H2CB-3-C6-IGFR		FDAVHGFDGGFYGFWKRELQR	15.7	7.8	10.2	0.8	1.3
H2CB-4-E11-IGFR		QAGGMEFHGAFYNWFLQLSG	26.1	17.6	24.1	0.7	1.4
H2CB-3-D6-IGFR		GRSVSRMNAEFYQWFGHQLAA	21.6	13.0	18.8	0.7	1.5
H2CB-4-F3-IGFR		AAVNSLFHDEFYLFWFQDLDG	17.3	11.1	16.4	0.7	1.5
H2CB-3-A4-IGFR		QLGMDWFHADFYEWFLAQLPS	27.4	11.0	14.8	0.7	1.3
H2CB-3-B1-IGFR		RLAGSGIHEGFYGFVFDQLLA	20.0	11.0	15.2	0.7	1.4
H2CB-3-C5-IGFR		GREIGGVHDGFYDWFRRQSEQ	19.9	10.5	15.6	0.7	1.5
H2CB-4-F6-IGFR		VRSEQRFDSSFYQWFNDLLMS	18.6	10.1	14.6	0.7	1.4
H2CB-3-B8-IGFR		QSPYGFHDFYRWFLQQTGM	20.7	6.9	9.5	0.7	1.4
H2CB-3-C7-IGFR		FQCGAAFHVDYRWFTCQEQF	16.2	1.8	2.5	0.7	1.4
H2CB-4-H7-IGFR		GAFGEFHEQFYRWFEALSF	21.8	14.1	22.7	0.6	1.6
H2CB-4-F5-IGFR		EHTSYQIHRQFYEWFDALGR	12.9	4.0	7.2	0.6	1.8
H2CB-4-G1-IGFR		SGTAADLHSRFYGFWALQARE	20.4	10.3	19.7	0.5	1.9
H2CB-3-D11-IGFR		EGFGVLFHGQFYRWFLQLDG	24.1	8.8	18.6	0.5	2.1
H2CB-3-D7-IGFR		QQSAGHPHSSFYLFWSLPGA	22.1	6.5	13.6	0.5	2.1
H2CB-3-C10-IGFR		YLQRAGFHRSFYGFWDQALRD	21.7	5.1	10.4	0.5	2.0
H2CB-4-E3-IGFR		MWLWATLHSDFYSWFEQVVS	20.3	4.6	8.9	0.5	1.9
H2CB-3-C1-IGFR		GANALGFKDRFYEWFAAQLWD	22.3	6.7	15.7	0.4	2.3
H2CB-4-G2-IGFR		GSGLYVFWHGFYDWFEEQMG	19.9	3.3	10.7	0.3	3.3
H2CB-3-A11-IGFR		LDKGWGFDDLQFYRWFEAATRA	23.9	2.5	7.7	0.3	3.1
H2CB-4-G5-IGFR		QRSAREFHADFYDWFLLRLTP	19.3	2.5	7.9	0.3	3.1
H2CB-4-F12-IGFR		DQRMGSFHGEFYRWFEETLLS	16.7	1.7	5.4	0.3	3.1

Figure 1N (Con't)

Clone	Design	Sequence X_n -Fy x WF- X_m	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-3-B11-IR		GRFYGNFQDAIDQLMPWGFDP	24.6	1.4	23.6	0.1	16.8
20E2B β -3-E3-IR		IQGWEPFYGFDDVVAQMFE	23.0	0.9	15.3	0.1	16.3
rB6-3-F6-IR		RYGRWGLAQQFYDWFDR	40.9	1.0	13.3	0.1	13.3
rB6-4-F9-IR		RGRGLSLSTQFYNWFAE	34.1	1.0	12.6	0.1	12.6
20E2B α -3-A8-IR		ASAYTPFYQWFADVVSEYMQQ	35.4	7.4	34.4	0.2	4.6
A6L-4-F6-IR		PYRMETEKWNFYDWFVAQLQ	28.9	4.1	18.1	0.2	4.4
20E2B α -4-H9-IR		SAVHFQFYKWFNDLLPVPLSA	37.8	9.4	26.7	0.4	2.9
20E2B α -3-B1-IR		VPVNKSFYRWFLVLGSDDW	41.8	12.9	36.8	0.4	2.9
20E2B β -4-F9-IR		QSPRASFYGFDDVLRAGVV	25.9	4.2	10.1	0.4	2.4
20E2B β -3-E9-IR		TGFYEWFEQLHSRMLPNPLD	27.0	7.7	17.2	0.5	2.2
20E2B β -3-E10-IR		RRGVGGFYGFWSQQLQGMVA	22.2	2.6	5.5	0.5	2.1
20E2B α -3-C12-IR		SSQDRRFYRWFEQAI VGGRDG	39.0	6.7	12.0	0.6	1.8
20E2B β -3-C12-IR		TRGQLGFYNWFQQALSTSGMG	20.2	2.2	3.8	0.6	1.8
20E2B β -3-E7-IR		CADLNAFYQWFCGVLDGRSDH	9.2	1.2	1.9	0.6	1.6
20E2B β -3-E11-IR		TLIQDQFYWNWFSDDL SAEFGD	20.7	1.3	2.1	0.6	1.6
20E2B α -3-B11-IR		IDQLDAFYRWFDDGVMGMGDP	36.0	20.7	32.8	0.6	1.6
NNKH-4-G2-IR		RGGGTFYEWFE SALKKHGAG	10.8	6.3	8.9	0.7	1.4
20E2B α -3-A7-IR		RGLDQDFYRWFNQNLVGVVEYDR	19.0	4.2	5.5	0.8	1.3
20E2B α -4-G12-IR		MQGHRGFYGNWFARVLEQDRGW	37.0	22.3	29.5	0.8	1.3
20E2B α -3-C11-IR		ERLHLRFYEWFDTVIGQDGS	37.3	26.8	34.8	0.8	1.3
20E2B α -3-C10-IR		MHVQSDFYHWFQSLLGQGGPD	37.7	24.8	30.5	0.8	1.2

Figure 10

Clone Design	Sequence $X_n - Fy \times WF - X_m$	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2B α -3-D7-IR	TMGTQGFYRWFNVVKEHLSG	35.4	26.9	31.3	0.9	1.2
20E2B α -3-A12-IR	ITHNRGFYSWFLDVVQGGAGA	31.7	22.0	23.3	0.9	1.1
20E2B α -3-D10-IR	VRRDAGFYQWFADILTQDFE	32.7	27.3	29.1	0.9	1.1
20E2B α -4-G7-IR	MQLQDEFYNWFRGIMLNDGQD	34.2	29.0	30.7	0.9	1.1
20E2B α -4-F5-IR	GIRSSGFYQWFDRLAGVGDG	33.8	32.1	34.0	0.9	1.1
20E2B α -3-C9-IR	ANLNSQFYSWFASVTGEASPS	39.4	33.2	35.5	0.9	1.1
20E2B α -3-A4-IR	QSPRASFYGWFDLRAAGVV	38.2	31.6	35.9	0.9	1.1
20E2B α -4-E12-IR	MQRNQGFSWFDDLSSTGV	36.0	30.8	29.7	1.0	1.0
20E2B α -4-E11-IR	ASGDFPFYAWFLEQLRVANGS	35.1	31.2	30.7	1.0	1.0
20E2B α -4-E8-IR	SGTPYGFYRWFSALASATSG	36.1	30.5	30.7	1.0	1.0
20E2B α -4-H10-IR	QGVGGFYEFWDRAVGDRPW	38.9	30.6	30.7	1.0	1.0
20E2B α -4-F6-IR	DNMSGFYRWFAQVVADSGD	34.9	33.2	32.0	1.0	1.0
20E2B α -4-G4-IR	RGTDFTFYGFQDQLQWCDD	34.1	33.7	32.2	1.0	1.0
20E2B α -4-F8-IR	TVDHTQFYDWFSLVGESGSA	37.7	32.0	32.7	1.0	1.0
20E2B α -4-G5-IR	GRQREFYWFELQAGGMDGD	34.9	33.9	33.4	1.0	1.0
20E2B α -3-B10-IR	RLLLGGFYEFWDQVLKETKEV	38.2	34.9	33.6	1.0	1.0
20E2B α -3-C7-IR	GVLSTGFYEFWALQLHGLAAG	37.6	34.2	34.8	1.0	1.0
20E2B α -3-C5-IR	PAVGQSFYGFWEAVLRGSKAG	40.4	36.0	35.6	1.0	1.0
20E2B α -3-B9-IR	SNGISGFYEFWAAQVQTSDFQ	39.6	35.8	37.1	1.0	1.0
A6L-4-F11-IR	LLGLSQAAAYANFYDWFVSQLA	33.1	4.6	4.6	1.0	1.0
20E2B α -3-C2-IR	VPNSWMFYNWFAEQIEGSEGE	44.1	40.0	38.1	1.0	1.0
20E2B α -3-B2-IR	ARRADGFYDWFREQVSGSAVQ	43.1	40.1	39.0	1.0	1.0
20E2B α -4-G2-IR	GVVEGTFYEFWFDRLGGVQGD	34.1	33.6	29.8	1.1	0.9
20E2B α -4-H6-IR	SHLTDPFYQWFDQLRAGVRG	39.4	36.0	31.9	1.1	0.9

Figure 10 (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
Design		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
R40-3-B6-IGFR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R40-X-E5-IGFR	AETPAQVGWNRLLWSVWPGEHWNTVDPFYHKLSELLRESGA	--	--	--	--	--
R40-X-B5-IGFR	RHLTNAELGVQSPEVLSRLFPDGDIFYRALSHLVRGMGPP	--	--	--	--	--
R40-4-9-IGFR	RGMDRQWLVDVGARHRLERRSVQDNTDDFYGGLRILVDGF	--	--	--	--	--
R40-3-G6-IGFR	GPPDSFDVTEKGDMAILNVRFDPHSLDFNDQTFYFLDLSL	--	--	--	--	--
R40-4-12-IGFR	GGTYFRGQVAQSNESLLRVNFLQLLEALAAPPT	--	--	--	--	--
R40-3-A5-IGFR	APFDARLSAPRFQWSPRTWXQSLSYGEWSCGSFYDCLSSI	--	--	--	--	--
R40-X-C6-IGFR	MGSSQFQDTRPSSGQAYSHSLDSDGWTANWIFLRALEGL	--	--	--	--	--
	SGAAHEGNQGRERSTHAAANINDHLPGDAGIWLGYSWLS	--	--	--	--	--

FIGURE 2B

[illegible]

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
Design	xxxxxxxxxxxxxxxxxxxx	--	--	--	--
R20-4-F11-IGFR	GFYELLGALVGERVGTGNS	39.0	19.2	--	--
R20-4-C7-IGFR	ERTDPFYKALLSLGGDGG	33.4	17.5	--	--
R20-3-F2-IGFR	DVQNGSSGFYDIGIFGLAWG	31.8	14.3	--	--
R20-4-A11-IGFR	PFYVWIRDLLGPELPHTRGD	37.8	13.5	--	--
R20-4-B12-IGFR	VLVVGGLDPFYEGLHRLIS	37.2	10.0	--	--
R20-4-B10-IGFR	GFYRLNLELVREGGALKVGA	37.0	9.5	--	--
R20-4-E9-IGFR	GQRFYELLSSELLGHEGGVF	34.2	9.4	--	--
R20-3-H4-IGFR	DWVSGPFYRGIELLSGFQIE	30.3	7.8	--	--
R20-3-G2-IGFR	GGSLFYEGLLRLVLGDSVVG	20.8	6.9	--	--
R20-4-B8-IGFR	LNHFYAMLSDSLGVRNIFPG	32.8	6.5	--	--
R20-4-E7-IGFR	LSGFYEGFLRLARRDGGWG	35.4	6.4	--	--
R20-4-G9-IGFR	FYDVL ¹ SALVGVELGEQGDAS	25.0	6.4	--	--
R20-4-D9-IGFR	GAGSFGREGGFYEALMQLAG	23.4	6.3	--	--
R20-4-D11-IGFR	DDEFYSQILKLVDGSRGGRSGTQN	31.3	4.0	--	--
R20-4-G10-IGFR	PFYMLLSRLVGGVEQEGGL	13.6	3.3	--	--
R20-4-C8-IGFR	FYDAIDQLVRGSARAGGTRD	16.8	3.2	--	--

FIGURE 2D

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-G3-IGFR	TFYSCLASLLTGTPQPNRGPWERC	33.1	32.3	1.2	27.0	<0.1
20C-4-C7-IGFR	FFYDCLAALLQGVARYHDLCAVEIT	35.3	28.0	1.3	21.8	<0.1
20C-3-F6-IGFR	DRDFCRFYERLTALVGGQVDGGWPC	33.5	26.1	1.9	14.1	0.1
20C-3-A1-IGFR	SSYGCDGFYLMFLSLGLVASQLEEC	26.5	20.8	1.5	13.7	0.1
20C-3-A4-IGFR	QFYGCLLDLSLGVPSFGWRRRCITA	17.7	8.8	1.2	7.6	0.1
20C-3-E4-IGFR	FFYRCLSRLLGGQLGSRGLSCIGD	37.7	7.7	1.3	6.0	0.2
20C-4-D11-IGFR	DLFYCMMQLATAGVGSGLGVPVCG	33.3	17.2	6.1	2.8	0.4
20C-4-F7-IGFR	CDFYCALSRLSGQPRDRMPNYPGTS	31.2	28.9	17.0	1.7	0.6
20C-3-B2-IGFR	GSACDGFYACLHALVQGPGEW	37.7	35.2	30.9	1.1	0.9

FIGURE 2E

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6L-4-C8-IR		AETPAQVGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGA	40.5	6.1	40.8	0.2	6.7
B6L-4-B7-IR		ANLRLR?VGNRL*SVWPGQWNTVDP?YQKLYELVRESGA	19.6	4.0	23.5	0.2	5.9
B6L-3-H1-IR		AETPAQVGWNRNLSVWPGEHWNIVDPFYHKLSELLRESGD	20.6	2.8	2.7	0.9	1.1
B6L-4-E12-IR		AETPAHVC*TVGGLFGRVNTWNTVDPFYAKLSELLRESGA	15.5	4.1	3.0	1.1	0.9
B6L-4-D8-IR		GQNSGSAWDGISLWSVWPGDVWNPDPFYHKLSELLRESGA	36.0	9.4	8.5	1.1	0.9
B6L-4-F7-IR		AEAPAQVGWNLQPGEHWITVDPFYHKLSELLRESGA	37.8	24.6	20.6	1.2	0.9
B6L-4-B11-IR		AETPAQVGWNLWSVWPGEH*NTVDPFYHKLSELLRESDG	5.5	2.0	1.6	1.3	0.8
B6L-4-B12-IR		AETPAQVGQNLWSVWPGEHWNVTDPFYQKLFELLRESGA	6.8	2.0	1.6	1.3	0.8
B6L-4-B8-IR		AETPAQVQNLWSVWPGELWNTVDPFYHKLSELLRESGA	36.4	18.7	14.2	1.3	0.8
B6L-4-E8-IR		T*QGETPAQVSLWPGEHWNVTDPFYHRLSELLRESGA	35.6	11.4	8.6	1.3	0.8
B6L-3-G6-IR		QGETPAQIGWNLWSVWPGEHWNVTDPFYHKLSELLRESGA	7.6	2.5	1.8	1.4	0.7
B6L-3-G5-IR		VDTPAQVGWNRNLSVWPGEHWYTDPPFYH*LSELLRESGA	11.5	2.0	1.4	1.4	0.7
B6L-4-E10-IR		AETSAQVGWQRLWSVWPGDHWSTLDPFYHKLSELLRESGA	14.8	3.2	2.2	1.5	0.7
B6L-4-F10-IR		*NSPRVGWNLWSVWPGEHWNVTDPFYHKLSELLRESGV	26.2	11.5	7.2	1.6	0.6
B6L-3-F3-IR		AETPAQIGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGP	36.0	17.1	10.1	1.7	0.6
B6L-4-A7-IR		ADTPAQVSGNRNLSVWPGDHPWNTVDPFYHKLSELLRESGA	11.6	3.4	1.9	1.8	0.6
B6L-4-G8-IR		AGTPAQVG*NRLWSVWPGEHWNVTDPFYHKLSELLRESGA	30.4	11.2	5.9	2.0	0.5
B6L-4-F8-IR		D*QAWSVWPGQHWNTIDPFYHKLSELLRESGA	35.6	12.8	7.2	2.0	0.5
B6L-4-G7-IR		AETLARVGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGA	33.5	12.9	6.4	2.3	0.4
B6L-3-F4-IR		AATRPQVGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGS	16.9	6.3	2.7	2.4	0.4
B6L-3-H4-IR		LTTPAQVGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGA	20.6	4.9	2.0	2.5	0.4
B6L-3-A6-IR		ADNPAQVGWNRNLSVWPGEH*NTVDPFYHKLSELLRESGA	22.4	6.3	3.2	3.2	0.3
B6L-4-D7-IR		AETPAQVGWNRNLSVWPGEHWNVTDPFYHKLSELLRESGA	14.3	4.8	1.4	3.4	0.3
B6L-3-E2-IR		AETSVQVGWIRLQSVWPGEHWNVTDPFYHKLSELLRGSGA	29.2	16.7	3.8	6.3	0.2
		G*NSAHVGWNRNLSVWPGEHWNVTDPFYHKLSELLRVSGG					

FIGURE 2F

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFsR/IR	IR/IGFsR
B6H α -3-F5-IR	OOUUUUUUJJJJPPFYHKLSELXXOO	42.7	9.6	17.9	0.5	1.9
B6H α -2-D10-IR	GGAVAAAVVGSRADPPFYHKLSELVQGS	20.8	1.7	1.1	1.5	0.6
B6H α -3-F1-IR	SGGGQQRKAIATSDDPFYHKLSELLGG	22.5	2.4	1.3	1.8	0.5
B6H α -3-E6-IR	CSMAAAEAGDDDDPPFYHKLSELQCGS	18.2	2.3	1.2	1.9	0.5
B6H α -1-B8-IR	CGAKMTGTPNDPPFYHKLSELLQRG	44.6	5.2	2.1	2.5	0.4
B6H α -2-D5-IR	CCVEAAEAVGRRGDPFYHKLSELTGCC	39.6	2.3	0.9	2.6	0.4
B6H α -1-B3-IR	SRVVTMVIKRGSPDPFYHKLSELVQGR	33.1	3.2	1.1	2.9	0.3
B6H α -3-E5-IR	GCITAENGAGDPFYHKLSELGGCS	28.8	2.9	1.0	2.9	0.3
B6H α -4-H9-IR	RCGDEEGWQENRRDDPFYHKLSELFQGC	17.4	6.4	2.1	3.0	0.3
B6H α -2-D8-IR	GCEVIAAEGRRDDPFYHKLSELQCGG	19.3	3.0	1.0	3.0	0.3
B6H α -3-E4-IR	SSETAKMVTGTRDDPFYHKLSELVQGS	43.1	8.7	2.8	3.1	0.3
B6H α -3-F7-IR	WLCDGGWKQRRPPGDPFYHKLSELIDCG	41.5	3.1	1.0	3.1	0.3
B6H α -1-A3-IR	SRVAATKEKRPSDDPFYHKLSELLQGS	37.4	2.6	0.8	3.3	0.3
B6H α -4-H10-IR	SRAKVEAEMPDSGDPFYHKLSELLASG	50.5	29.5	8.6	3.4	0.3
B6H α -3-F6-IR	GGAAKTTVVGSPPDDPFYHKLSELLQGS	48.9	19.7	5.7	3.5	0.3
B6H α -3-F3-IR	CGVGEQMEVTDGDDPFYHKLSELLWSC	18.1	15.6	4.3	3.6	0.3
B6H α -4-G8-IR	SGEQTATIEGPSNDPFYHKLSELIWGS	32.3	6.1	1.7	3.6	0.3
B6H α -2-D1-IR	GGTKAVAKVGTDRDDPFYHKLSELLQGS	11.7	5.4	1.3	4.2	0.2
B6H α -3-E7-IR	GCEVIVEEGDSADPFYHKLSELQCGS	47.0	5.6	1.3	4.3	0.2
B6H α -2-D6-IR	GCAVVEEAERSRGDPFYHKLSELIQGC	33.5	4.4	1.0	4.4	0.2
B6H α -3-F10-IR	GRTMAVMAAGGDDPFYHKLSELVQGG	47.2	8.8	1.9	4.6	0.2
B6H α -3-E8-IR	GCVVEWQKWHGASDPFYHKLSELGGCS	47.6	5.3	1.1	4.8	0.2
B6H α -2-C10-IR	RGKTAAVIVGRPADPFYHKLSELLQGG	46.9	5.8	1.1	5.3	0.2
B6H α -2-C7-IR	SGAKVIVVTGSDGDPFYHKLSELLQGS	45.1	6.7	1.0	6.7	0.1
	RGIVAMVEATEVGSDDHDPFYHKLSELVQGS					

FIGURE 2H

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	OOUUUUUUJJJJPPFYHKLSELXXOO	--	--	--	--	--
B6H α -1-A6-IR	GCKMEETETGTSDDPFYHKLSELCSGG	49.7	34.5	4.0	8.6	0.1
B6H α -2-C5-IR	RGEVATMEVPAGDPFYHKLSELLWGS	42.6	34.2	3.3	10.4	0.1
B6H α -2-C4-IR	RCGRW*AEMGAGDDPFYHKLSELVCG	20.7	9.9	0.9	11.0	0.1
B6H α -2-C9-IR	RCMVETIAGSGDDPFYHKLSELQCGG	47.4	32.6	2.8	11.6	0.1
B6H α -4-H8-IR	WWQKSGDGASASDPFYHKLSELIWGS	36.3	28.1	2.4	11.7	0.1
B6H α -3-F11-IR	RGMKEEVLVGGSTDPFYHKLSELLOGS	49.5	18.7	1.6	11.7	0.1
B6H α -3-E9-IR	RCEEKQAEVGPSSDPFYHKMSELLGCR	44.6	24.2	1.7	14.2	0.1
B6H α -1-A2-IR	RGCNDDGGKGSDDPFYHKLSELICGG	22.3	14.6	1.0	14.6	0.1
B6H α -1-B5-IR	CCTTEMVMDARDDPFYHKLSELVTGG	41.5	20.5	1.0	20.5	0.0
B6H β -3-G4-IR	GCKKVEAKKGNADPFYHKLSELLQGC	36.4	28.4	36.0	0.8	1.3
B6H β -3-A10-IR	RSMMAKAIVGGPGDPFYHKLSELYELQFGR	36.7	27.9	34.7	0.8	1.2
B6H β -3-D9-IR	CGGAVPDGDDPFYHKLSELMQGC	34.9	32.1	35.6	0.9	1.1
B6H β -3-A3-IR	GCEEVEAETTGHRDPFYHKLSELLQGC	36.3	33.7	37.3	0.9	1.1
B6H β -3-G1-IR	GCAEIEIAAGGGDPFYHKLSELLQGC	34.7	33.7	35.9	0.9	1.1
B6H β -3-B3-IR	GCAEVKAVKGAGDDPFYHKLSELLQGC	35.9	35.1	37.4	0.9	1.1
B6H β -3-G11-IR	GCAAVETTNGRNDPFYHKLSELLQGC	37.6	36.2	39.0	0.9	1.1
B6H β -3-F5-IR	CGEVTGRAGDPFYHKLSELLQGC	39.2	37.2	41.0	0.9	1.1
B6H β -3-A1-IR	GCAMVEATEGRRHDPFYHKLSELIQGC	41.3	38.0	43.0	0.9	1.1
B6H β -3-H3-IR	GCTEVVSGDDPFYHKLSELLQGC	39.0	38.3	40.7	0.9	1.1
B6H β -3-D3-IR	GQCAMEEIIRGANDPFYHKLSELCEGG	38.8	38.4	41.3	0.9	1.1
B6H β -3-C9-IR	GCAEIVIEEGDDSDPFYHKLSELLQGC	36.7	39.2	41.5	0.9	1.1
B6H β -3-F1-IR	PQCSSIKAEGGSDPFYHKLSELLVGC	41.5	40.0	42.2	0.9	1.1
B6H β -3-C6-IR	GCAAVVAEASGDDPFYHKLSELLQGC	39.9	40.3	42.7	0.9	1.1

FIGURE 2H (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6Hβ-3-D7-IR	OOUUUUUUJJJDPPFYHKLSELXXOO	--	--	--	--	--
B6Hβ-3-B2-IR	RGVEMKAI VVGTPNDPPFYHKLSELSSGS	39.5	27.1	26.3	1.0	1.0
B6Hβ-3-G5-IR	CSAVKMAEAGDPSDPFYHKLSELCOGS	34.3	34.4	35.4	1.0	1.0
B6Hβ-3-H1-IR	RGDGDPPFYHKLSELMOSS	35.3	35.0	35.6	1.0	1.0
B6Hβ-3-A5-IR	WLCKRQTHTDPPFYHKLSELACGR	36.8	35.4	36.5	1.0	1.0
B6Hβ-3-H11-IR	SSKVVKATVGTGPHDPFYHKLSELQGS	34.9	35.5	35.9	1.0	1.0
B6Hβ-3-C2-IR	GCAAIAVATGNDNDPPFYHKLSELQGR	37.7	36.4	37.6	1.0	1.0
B6Hβ-3-C8-IR	GCAAVVKETHDPPDPFYHKLSELHGC	37.4	36.5	37.2	1.0	1.0
B6Hβ-3-A11-IR	SCAAEKEVAGTARDPPFYHKLSELMOSS	37.0	37.7	39.5	1.0	1.0
B6Hβ-3-B7-IR	CSVAVGDSGDPFYHKLSELQGR	40.4	38.2	39.1	1.0	1.0
B6Hβ-3-B4-IR	WQRNKQIIIGTPDDPPFYHKLSELLEGS	35.4	38.3	39.5	1.0	1.0
B6Hβ-3-A4-IR	RSAAAKAVIGSPNDPPFYHKLSELIQGG	37.8	39.0	39.4	1.0	1.0
B6Hβ-3-E12-IR	WLCDRDGRDEQPDPPFYHKLSELVSCGR	33.5	39.4	41.3	1.0	1.0
B6Hβ-3-B8-IR	GSVAAAKKTGSSDDPPFYHKLSELQGS	39.0	39.8	41.1	1.0	1.0
B6Hβ-3-C5-IR	GCAVTTMTMRSPADPPFYHKLSELQGR	40.1	40.4	41.1	1.0	1.0
B6Hβ-3-A2-IR	GCKVDDE*ARSSDPFYHKLSELKGCGR	35.8	40.7	40.7	1.0	1.0
B6Hβ-3-A8-IR	GCKAVVEVKDHGDDPPFYHKLSELQGC	40.8	40.7	39.5	1.0	1.0
B6Hβ-3-B11-IR	CSTVTVSGSDDPPFYHKLSELQGC	40.7	40.9	42.6	1.0	1.0
B6Hβ-3-B5-IR	RSVTAKVEVGSDRDPFYHKLSELQGS	41.1	41.4	41.9	1.0	1.0
B6Hβ-3-C4-IR	GSRRQKIEVGTNDPPFYHKLSELQGG	40.0	41.9	41.6	1.0	1.0
B6Hβ-3-G7-IR	LCDEKQRTVTGTDNDPPFYHKLSELTGGR	39.8	42.0	41.3	1.0	1.0
B6Hβ-3-C11-IR	SCMVEGPNDDPPFYHKLSELQGR	40.7	42.6	43.3	1.0	1.0
B6Hβ-3-B5-IR	GGAUVVAMGNDPPFYHKLSELQGG	43.0	42.7	44.0	1.0	1.0
B6Hβ-3-C4-IR	GGVIKAMKAGPDDPPFYHKLSELQGS	42.7	43.9	45.4	1.0	1.0
B6Hβ-3-G7-IR	GCIIAEKVVGPDDPPFYHKLSELDCG	41.1	42.3	36.6	1.2	0.9
B6Hβ-3-C11-IR	GCEKVVAVAGNAGDPPFYHKLSELQGC	4.1	2.4	2.1	1.1	0.9
B6Hβ-3-C11-IR	GSVMVTVMAGADDPFYHKLSELQGGGR	29.2	30.6	28.2	1.1	0.9

FIGURE 2H (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6Hβ-3-H12-IR	OOUUUUUUJJJDPFYHKLSELXXOO	--	--	--	--	--
B6Hβ-3-G10-IR	RGEAKEAKIGSAGDPFYHKLSELMQGSR	33.6	32.0	29.5	1.1	0.9
B6Hβ-3-F10-IR	GCEVVVMANSSADPFYHKLSELCOGSR	30.1	34.3	30.5	1.1	0.9
B6Hβ-3-D5-IR	GCAAVVTTGGDNDPFYHKLSELLQGCR	37.1	35.3	32.4	1.1	0.9
B6Hβ-3-B12-IR	SRTGERQVVGSHADPFYHKLSELLLS	39.9	38.9	35.5	1.1	0.9
B6Hβ-3-D2-IR	GCKEVVETAHADDPFYHKLSELLQGCR	39.5	40.0	37.1	1.1	0.9
B6Hβ-3-D1-IR	RRITIKVKAGDDDDPFYHKLSELLWGG	40.4	41.5	39.1	1.1	0.9
B6Hβ-3-G6-IR	WCDQKETVVSNSDDPFYHKLSELVGC	41.1	44.6	36.6	1.2	0.8
B6Hβ-3-A7-IR	RCEEITIGDGRAGDPFYHKLSELLQGC	34.3	36.4	24.1	1.5	0.7
B6Hβ-3-B10-IR	CSVVMTTEKNDRDDPFYHKLSELLQGC	38.1	30.9	18.4	1.7	0.6
B6Hβ-3-B9-IR	GGEARRRQQVGTANDPFYHKLSELAFGGR	32.3	36.5	22.8	1.6	0.6
B6Hβ-3-D6-IR	GCAVTAITINGTSDPFYHKLSELCOGS	38.6	38.5	20.8	1.9	0.5
B6Hβ-3-C7-IR	GSKVKAMAVGTSDDPFYHKLSELVQGR	35.9	36.0	15.6	2.3	0.4
	RCKGIKAHSDNDPFYHKLSELCOGG	38.3	38.0	6.6	5.8	0.2

FIGURE 2H (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR IR	IGFR/IR	IR/IGFR
B6H-3-F1-IGFR	OOUUUUUUJJJJDPFYHKLSELLXXOO	--	-- --	--	--
B6H-3-D4-IGFR	RRVAAVA?KDATGDPFYHKLSELLRS	20.0	30.8	--	--
B6H-3-G3-IGFR	RSTMKEKIEGDNDPFYHKLSELLKSG	19.0	27.6	--	--
B6H-3-F2-IGFR	GGAVIVTAARRGSDPFYHKLSELVGR	14.2	25.2	--	--
B6H-3-D1-IGFR	SREAVEVTMARGSDPFYHKLSELVWGS	12.5	24.8	--	--
B6H-3-A3-IGFR	RSTTMVKAVPPRPDPFYHKLSELL*GG	20.0	24.2	--	--
B6H-3-A4-IGFR	GRTEEVVVGTTRDPFYHKLSELLASG	14.2	22.8	--	--
B6H-3-B4-IGFR	RRMAGWQ*TSSSDPFYHKLSELVSGS	13.0	22.8	--	--
B6H-4-D11-IGFR	SRKEVTEMVGGSPDPFYHKLSELMGSG	10.2	22.8	--	--
B6H-3-G2-IGFR	RGTAQRKSSDP*DPFYHKLSELIYGS	14.0	22.5	--	--
B6H-3-B2-IGFR	GGVAVVAARRDDPFYHKLSELVSGR	15.2	22.5	--	--
B6H-3-E2-IGFR	SR.MAMVEVGNPGDPFYHKLSELLGS	14.5	21.9	--	--
B6H-3-B1-IGFR	RRVTAVIEVDGADDPFYHKL?ELLSSG	11.6	21.8	--	--
B6H-4-G3-IGFR	RSVIAN??G?NADPFYHKLSELISSG	15.9	21.7	--	--
B6H-4-F9-IGFR	RGVVIETTKDPGADPFYHKLSELLFGR	19.1	21.4	--	--
B6H-3-E3-IGFR	RRTTVMEIVGGRDDPFYHKLSELLHRG	11.3	20.9	--	--
B6H-3-E1-IGFR	GRVVAAAARPDPPFYHKLSELVAGR	14.2	20.8	--	--
B6H-4-F3-IGFR	RGVATVVVANHHSDPFYHKLSELVLRG	20.0	20.6	--	--
B6H-3-D2-IGFR	RRKMATEIMRSDADPFYHKLSELLGGS	12.5	20.3	--	--
B6H-4-A9-IGFR	GGKTAVEVTS PASDPFYHKLSELLLRG	12.1	19.3	--	--
B6H-4-E6-IGFR	RREKKVVTITDNDPFYHKLSELVFGG	14.1	19.2	--	--
B6H-4-C3-IGFR	SSAII MVAADRADDPFYHKLSELLWGS	12.5	19.2	--	--
B6H-3-C2-IGFR	RRVAIVAAAGAGGDPFYHKLSELLSRG	23.6	18.9	--	--
B6H-3-C4-IGFR	RRMVMEAAENHADDPFYHKLSELLWRD	16.2	18.5	--	--
B6H-3-C3-IGFR	GRKMEIVAIRGAHDPFYHKLSELL*GR	16.8	17.2	--	--
B6H-3-B3-IGFR	CCIAMVEMAAGGGDPFYHKLSELLSGR	14.6	17.1	--	--
B6H-4-H3-IGFR	RGAQSPDPFYHKLSELAFGS	9.0	16.8	--	--
B6H-3-H3-IGFR	RKTAMVVI GDASDPFYHKLSELAFGS	10.1	16.6	--	--
	GSVITKAMKADGGDDPFYHKLSELL*GG	14.2	16.4	--	--

FIGURE 21

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
B6H-4-D8-IGFR	OOUUUUUUJJJJDPFYHKLSELXXOO	15.1	16.4	--	--
B6H-4-D6-IGFR	GGVKA AAAERDDSDPFYHKLSELFGS	12.6	15.6	--	--
B6H-4-E10-IGFR	CCEMVKTIEHGGNDPFYHKLSELVFR	10.2	15.1	--	--
B6H-4-F5-IGFR	GGAKVAVVVDHGDDPFYHKLSELGRS	12.3	14.8	--	--
B6H-4-B2-IGFR	RGKTKMAAAGNRDPFYHKLSELI FGN	6.6	11.8	--	--
B6H-3-F3-IGFR	SGEGEMAMPGDDPFYHKLSELIGRA	8.2	11.6	--	--
B6H-3-A2-IGFR	GGMAEVVVVGPPRDPFYHKLSELVGG	10.9	9.9	--	--
B6H-3-H2-IGFR	GGEVKVMVADGSTDPFYHKLSEL LGRT	5.9	9.6	--	--
B6H-4-A1-IGFR	SCVMVETVAGNRDPFYHKLSELVGGC	4.4	9.5	--	--
B6H-3-H1-IGFR	RRW* KVPGAADPFYHKLSELGRSA	7.2	8.7	--	--
B6H-4-C2-IGFR	GGVEATEVEHADGDPFYHKLSELVGRS	6.7	8.6	--	--
B6H-4-H9-IGFR	RGVEVAVITHGPPDPFYHKLSEL LRG	12.3	8.4	--	--
B6H-4-B7-IGFR	SGTVTVIAMSGTDDPFYHKLSEL LRS	6.4	8.2	--	--
B6H-4-A7-IGFR	GRTAVVKEASPAHDPFYHKLSEL LRG	9.7	8.1	--	--
B6H-4-B3-IGFR	RGAIGNAAVGNRSDPFYHKLSELISRG	4.4	7.8	--	--
B6H-4-B4-IGFR	GGMIKTAMEHDTDPFYHKLSEL LRG	5.2	7.4	--	--
B6H-4-E1-IGFR	GCAEEVEVAGAGHDPFYHKLSEL CAGG	3.6	7.1	--	--
B6H-3-C1-IGFR	SSVVVVEVVDARRDPFYHKLSELV?SG	5.7	4.6	--	--
B6H-4-A3-IGFR	GRKKAVATMTDGGDPFYHKLSELILRS	4.4	4.2	--	--
B6H-4-H10-IGFR	RGETEMAVADTDDDPFYHKLSEL LRG	4.4	3.2	--	--
B6H-3-G1-IGFR	GQRDPFYHKLSELMGRGA	2.4	2.9	--	--

FIGURE 21 (Con't)

Clone	Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
B6C-3-C7-IR		EHWNTVDPFYHKLSSELLRESG	--	--	--	--	--	--
B6C-4-F2-IR		EHWNTVDPFYFTLFE*LRESG	31.7	2.1	20.0	0.1	9.4	
B6C-3-A2-IR		EHWNTVDPFYNQWLWELRESG	8.2	1.8	4.3	0.4	2.4	
B6C-4-H11-IR		EHWNTVDPFYHQLSWELRESG	34.9	18.1	36.0	0.5	2.0	
B6C-4-H4-IR		EHWNTVDPFYQQLYEWELRESG	37.1	28.2	38.6	0.7	1.4	
B6C-3-A11-IR		EHWNTVDPFYRQLSEWELRESG	39.5	28.3	39.4	0.7	1.4	
B6C-3-D9-IR		EHWNTVDPFYHYFQELRESG	25.4	25.9	34.2	0.8	1.3	
B6C-4-G4-IR		EHWNTVDPFYHQMYEWELRESG	35.7	30.3	37.2	0.8	1.2	
B6C-3-C6-IR		EHWNTVDPFYRQLYEWELRESG	35.3	31.0	38.4	0.8	1.2	
B6C-3-D8-IR		EHWNTVDPFYGLQELRESG	33.3	33.9	35.9	0.9	1.1	
B6C-4-G7-IR		EHWNTVDPFYH*ISELLRESG	34.5	34.7	37.1	0.9	1.1	
B6C-3-C8-IR		EHWNTVDPFYQFAELLRESG	35.9	36.9	38.9	0.9	1.1	
B6C-3-D6-IR		EH*NTVDPFYEGLELLRESG	35.6	37.2	39.6	0.9	1.1	
B6C-3-C10-IR		EH*NTVDPFYQGLFELLRESG	37.6	37.6	40.2	0.9	1.1	
B6C-3-B3-IR		EHWNTVDPFYQYFSELLRESG	35.3	36.4	40.6	0.9	1.1	
B6C-3-B1-IR		EHWNTVDPFYGLQTLRESG	38.3	38.7	40.8	0.9	1.1	
B6C-4-F6-IR		EHWNTVDPFYQALFELLRESG	37.8	38.9	41.2	0.9	1.1	
B6C-3-B11-IR		EHWNTVDPFYD*MRNLLRESG	35.8	36.8	38.7	1.0	1.1	
B6C-3-B8-IR		EHWNTVDPFYNLLQELRESG	36.3	37.0	38.8	1.0	1.1	
B6C-3-C12-IR		EHWNTVDPFYDGLRQLRESG	37.2	39.2	41.2	1.0	1.1	
B6C-3-C2-IR		EHWNTVDPFYGKLQELRESG	28.3	28.7	28.9	1.0	1.0	
B6C-3-D5-IR		EHWNTVDPFYQQLFELLRESG	34.1	34.7	33.8	1.0	1.0	
B6C-4-F7-IR		EHWNTVDPFYMLQQLRESG	33.9	35.3	34.1	1.0	1.0	
B6C-4-H2-IR		EH*NTVDPFYHKLYELLRESG	34.9	34.7	34.2	1.0	1.0	
B6C-3-B12-IR		EHWNTVDPFYH*MSNLLRESG	35.4	35.8	35.8	1.0	1.0	
B6C-3-A12-IR		EHWNTVDPFY*MSSELLRESG	33.6	35.2	36.0	1.0	1.0	
B6C-4-E9-IR		EHWNTVDPFYQLLPELLRESG	33.1	37.0	36.2	1.0	1.0	
B6C-4-E8-IR		EHWNTVDPFYQRMPELLRESG	36.1	36.0	36.2	1.0	1.0	
		EHWNTVDPFYQGLWELLRESG	34.2	35.0	36.6	1.0	1.0	

FIGURE 2J

01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6C-4-F4-IR	EHWNTVDPPFYHKLSELLRESG	--	--	--	--	--
B6C-3-D2-IR	EHWNTVDPPFYQKLFE ^u LLRESG	36.3	36.9	34.3	1.1	0.9
B6C-3-A1-IR	EHWNTVDPPFYH*LAELLRESG	8.5	10.3	9.0	1.2	0.9
B6C-3-B5-IR	EHWNTVDPPFYH*LNELLRESG	26.5	30.7	16.8	1.8	0.5
B6C-3-A4-IR	EHWNTVDPPFYHKLQELLRESG	33.4	33.0	15.0	2.2	0.5
	EHWNTVDPPFYRRLLQELLRESG	33.6	31.8	13.5	2.4	0.4

FIGURE 2J (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6C-3-C4-IGFR	EHWNTVDPFYYHKLSELLRESGA	--	--	--	--	--
B6C-3-F5-IGFR	EHWNTVDPFYLKMTPELLRESGA	21.0	23.1	--	--	--
B6C-3-D4-IGFR	EHWNTVDPFYYHKLSELLRESGA	26.5	22.6	--	--	--
B6C-3-A3-IGFR	EHWNTVDPFYYHKLSELLRESGA	26.6	22.1	--	--	--
B6C-3-C9-IGFR	EHWNTVDPFYYHKLSELLRESGA	29.7	20.8	--	--	--
B6C-3-C8-IGFR	EHWNTVDPFYYHKLSELL?ESGA	29.6	20.5	--	--	--
B6C-3-A8-IGFR	EHWNTVDPFYYHKLSELLRESGA	30.5	19.9	--	--	--
B6C-3-A2-IGFR	EHWNTVDPFYYHKLSELLRESGA	29.7	19.7	--	--	--
B6C-3-A9-IGFR	EHWNTVDPFYYHKLSELLRESGA	33.6	19.0	--	--	--
B6C-3-C10-IGFR	EHWNTVDPFYYHKLSELLRESGA	33.0	18.3	--	--	--
B6C-3-F7-IGFR	EHWNTVDPFYYHKLSELLRESGA	30.0	17.7	--	--	--
B6C-3-F10-IGFR	EHWNTVDPFYYHKLSELLRESGA	27.3	17.6	--	--	--
B6C-3-C12-IGFR	EHWNTVDPFYYHKLSELLRESGA	27.4	17.4	--	--	--
B6C-3-E11-IGFR	EHWNTVDPFYYHKLSELLRESGA	28.4	17.3	--	--	--
B6C-3-F8-IGFR	EHWNTVDPFYYHKLSELLRESGA	28.0	17.2	--	--	--
B6C-3-F2-IGFR	EHWNTVDPFYYHKLSELLRESGA	25.4	16.0	--	--	--
B6C-3-B6-IGFR	EHWNTVDPFYYHKLSELLRESGA	30.8	15.1	--	--	--
B6C-3-D5-IGFR	EHWNTVDPFYYHKLSELLRESGA	2.9	14.7	--	--	--
B6C-3-A4-IGFR	EHWNTVDPFYYHKLSELLRESGA	2.4	14.3	--	--	--
B6C-3-D3-IGFR	EHWNTVDPFYYHKLSELLRESGA	22.6	13.9	--	--	--
B6C-3-F9-IGFR	EHWNTVDPFYYHKLSELLRESGA	28.0	13.8	--	--	--
B6C-3-A7-IGFR	EHWNTVDPFYYHKLSELLRESGA	24.8	13.6	--	--	--
B6C-3-H10-IGFR	EHWNTVDPFYYHKLSELLRESGA	14.4	12.8	--	--	--
B6C-3-H11-IGFR	EHWNTVDPFYYHKLSELLRESGA	17.1	11.1	--	--	--
B6C-3-A1E-IGFR	EHWNTVDPFYYHKLSELLRESGA	2.3	11.0	--	--	--
B6C-3-E12-IGFR	EHWNTVDPFYYHKLSELLRESGA	23.3	10.5	--	--	--
B6C-3-H12-IGFR	EHWNTVDPFYYHKLSELLRESGA	2.7	10.1	--	--	--
B6C-3-G1-IGFR	EHWNTVDPFYYHKLSELLRESGA	2.3	9.9	--	--	--
	EHWNTVGAFOPTPEYLLRESGA	--	--	--	--	--

FIGURE 2K

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
Design	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--
Parental	FYDAIDQLVGRSARAGGTRD	30.6	15.1	4.2	0.3
20E2A-4-F9-IR	PPWGARFYDAIEQLVFDNLCC	19.9	1.2	13.9	0.1
20E2A-4-E2-IR	IGRVRSFYDAIDQLFQSDWER	13.9	1.3	9.7	0.1
20E2A-3-B6-IR	RDAGSSFYDAIDQLVCLTYFC	14.5	1.6	6.1	0.3
20E2A-3-A7-IR	MPMGLNFYDGIQLVREWGDD	18.6	4.2	15.2	0.3
20E2A-4-F7-IR	TISAHTFYEAIQYIEGIDPL	20.1	10.6	15.8	0.7
20E2A-3-C9-IR	SPWGRAFYDALDQLMGAERG	24.4	16.4	23.8	0.7
20E2A-3-C11-IR	LSPPRDFYDAIQQLVVRDGGWG	14.8	5.9	6.6	0.9
20E2A-4-G7-IR	HGVPRTFYDAIDQLVWGIEVG	17.2	8.3	8.9	0.9
20E2A-4-H11-IR	GGTDQLFYGAIDQLVGGTWWR	25.4	26.9	25.6	1.1
20E2A-4-E9-IR	LSVHQSFYDAINEILFSGLEA	4.7	2.1	2.1	1.0
20E2A-4-F4-IR	GDARDPFYDAMEQLVYGEELGG	12.6	5.6	5.7	1.0
20E2A-3-A3-IR	VASPRSFYEAIAQLVFNLGQE	21.0	11.9	12.1	1.0
20E2A-4-E4-IR	RKPCQTFYDCILDLVVTDVDV	21.0	16.0	16.1	1.0
20E2A-4-G5-IR	LLSRWTFYDAIEQLVGGGADG	22.1	19.5	18.8	1.0
20E2A-4-H1-IR	PAGCQGFVEAIEQLVTGCECG	24.4	20.4	21.2	1.0
20E2A-3-D8-IR	AVFPRTFYEAIDQLVGVSLLG	22.3	20.8	20.3	1.0
20E2A-4-F11-IR	APIPFSFYDAIVQLVMQGDHE	23.2	21.0	20.4	1.0
20E2A-3-C1-IR	QCNPRTFYEAIAQLVTGCDVS	23.4	22.3	22.5	1.0
20E2A-3-B2-IR	VSTSGSFYDAIQQLLEDSSGW	24.6	22.5	22.8	1.0
20E2A-4-G10-IR	HHSAFSFYDAIAQLVGVPEEE	21.5	22.9	22.2	1.0
20E2A-3-A5-IR	FTYVHSFYDAIEQLVVRGEGGG	24.6	23.4	22.6	1.0
20E2A-4-H3-IR	QGNNAQNFYDAIDQLCFGCCLGG	24.5	24.1	25.1	1.0
20E2A-3-C4-IR	SSEGWTFFYDAIDQLVGRERGW	25.2	24.4	24.7	1.0
20E2A-4-E3-IR	PDGCATFYHAIQQLVTGFPCV	18.5	15.7	13.6	1.2
20E2A-4-E7-IR	RGPPMTFFYDAIAQLVAQSADG	17.8	16.6	14.4	1.2

FIGURE 2L

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-3-B3-IR	XXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-4-B10-IR	RSSCQSFYDAIERLVLGTCG	22.4	18.6	15.9	1.2	0.9
20E2A-4-F8-IR	VSRKFSFYDAIQQLVRGDAGV	24.8	24.5	21.2	1.2	0.9
20E2A-4-H5-IR	FORTWSFYDAINQLVMEGSGD	4.3	2.2	2.1	1.1	0.9
20E2A-4-G1-IR	RGSATTFYDAINQLVGQDGGW	21.3	18.3	16.5	1.1	0.9
20E2A-4-F2-IR	AQPCVSFYDAIEQLVTGRSCM	21.4	18.3	16.0	1.1	0.9
20E2A-4-H7-IR	GGDGPFFYDWIEQLVRAGSEA	20.1	20.5	18.2	1.1	0.9
20E2A-3-D5-IR	LDLCASFYDAIEQLVGKFCG	22.6	21.2	18.6	1.1	0.9
20E2A-3-A1-IR	WLACQSFYDAIDQLINGECN	22.7	21.3	18.9	1.1	0.9
20E2A-4-H9-IR	EVNALSFYDAIDQLVRGGLGG	23.8	21.7	19.9	1.1	0.9
20E2A-3-D7-IR	RLQPRTFYEAIDQLIGVLEG	24.0	22.5	20.8	1.1	0.9
20E2A-4-E5-IR	SGAHRTFYDAIQELVGMGSK	24.1	23.5	21.0	1.1	0.9
20E2A-4-E11-IR	NMQSLTFYDAIAQLVLRSGG	24.1	23.5	20.9	1.1	0.9
20E2A-3-A4-IR	RAVGATFYDQINQLVRKDDGY	22.5	14.6	11.7	1.3	0.8
20E2A-4-G8-IR	SQCRGGFYDAIYQLVTGVNCI	20.2	17.5	13.4	1.3	0.8
20E2A-3-B7-IR	DRLAFSFYDAIDQLVHCCGHG	21.7	18.0	13.8	1.3	0.8
20E2A-4-G11-IR	GNRQRFYDAIDQLVGGSWWR	21.1	21.4	16.9	1.3	0.8
20E2A-3-C5-IR	GGSVLSFYDAIAQLVGGQSI	22.9	23.1	17.7	1.3	0.8
20E2A-4-E8-IR	RSGPMSFYDAIEQLVGLRHP	24.2	24.3	19.0	1.3	0.8
20E2A-4-H2-IR	VSGCRTFYDAIDQLVSGQACG	17.1	11.5	9.4	1.2	0.8
20E2A-4-H4-IR	AQFPRTFYDAIEQLIHGKMD	21.6	13.7	11.6	1.2	0.8
20E2A-3-D4-IR	CAQPESFYDAIDRLVTGRCLV	21.3	19.6	16.3	1.2	0.8
20E2A-4-F5-IR	PDECQSFYCAIDRLVTGKGR	23.2	22.2	18.0	1.2	0.8
20E2A-3-B10-IR	QRRARDFYEAIQQLVGGVAGL	12.2	5.7	3.8	1.5	0.7
20E2A-3-B9-IR	PLVRGTFYDAIKQLVMGSSD	14.9	5.9	3.9	1.5	0.7
20E2A-3-D10-IR	VGIATFYDAIQQLVRGSPEG	15.5	11.0	7.2	1.5	0.7
20E2A-3-D6-IR	PRGQASFYDMIEQLVGSADWN	22.2	19.1	12.8	1.5	0.7
20E2A-4-G9-IR	DGRVWSFYDALEQLVGQFEGP	21.8	19.3	13.0	1.5	0.7
20E2A-4-E1-IR	RFVRSFYDAIEQLILAPNLG	21.3	19.9	13.3	1.5	0.7
20E2A-4-F12-IR	KVGRGSFYDAIRELVGQGHV	23.1	20.7	13.6	1.5	0.7
20E2A-4-G3-IR	PAIGFTFYDAIRQLVWFQCAD	17.5	17.1	12.1	1.4	0.7
	ALPGRSFYDAIAQLVGPDWGA	21.6	19.4	14.1	1.4	0.7

FIGURE 2L (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20E2A-3-C2-IR	XXXXXXFYDAIDQLVXXXXXX	23.4	20.9	15.4	1.4
20E2A-3-B1-IR	RPQGGTFYDMIKQLVLSGWG	22.1	21.6	15.6	1.4
20E2A-3-A8-IR	WSAFADFYDAIQHLVAGEVGA	12.3	4.8	2.7	1.8
20E2A-4-G2-IR	SDGRDGFYDAIQQLVRSFGD	18.9	13.8	7.9	1.8
20E2A-3-A9-IR	IRSVFSFYDAIDQLVKGGS	23.3	20.3	11.3	1.8
20E2A-3-D3-IR	GGVSLTFYEAIEQLVGGFDA	24.4	24.5	13.5	1.8
20E2A-3-A11-IR	AAQAFSFYDLINQLVASKPSE	13.5	4.6	2.7	1.7
20E2A-3-B4-IR	QSGACGFYDAINQLVLSVIC	21.4	15.3	8.9	1.7
20E2A-4-E10-IR	GGIVFSFYEAIDQLVRNGAG	22.3	19.0	11.3	1.7
20E2A-3-D2-IR	IYTGQGFYDAIEQLVRGGSTP	22.5	19.0	11.2	1.7
20E2A-4-F1-IR	KSPALSFYDAIEQLVGSQVGR	14.5	6.2	3.9	1.6
20E2A-3-D1-IR	ISPPWTFYDAIDQLVGGSDGR	16.5	6.6	4.0	1.6
20E2A-3-D11-IR	GSFRGFYDAIDQLVRQGLE	20.2	14.4	8.9	1.6
20E2A-3-C3-IR	GVAGGTFYDAIEQLVRQFGS	23.9	22.5	14.2	1.6
20E2A-3-C12-IR	RPLRWSFYDALDQLVGS AIGG	21.3	23.0	14.4	1.6
20E2A-3-A2-IR	MQRRGGFYDAIADLVGGHVRG	18.9	11.6	7.5	1.5
20E2A-3-C7-IR	TSQGLSFYDAINQLVAGCWGG	21.6	15.1	6.9	2.2
20E2A-3-C10-IR	SGGTVTTFYDAINQLVQGRYNG	18.1	18.0	9.1	2.0
20E2A-3-D9-IR	GGALDPFYDAIYQLVIRGSSG	21.8	21.6	8.4	2.6
20E2A-3-B5-IR	KQRGVTFYDLNQLVGG SARG	24.3	18.1	7.4	2.5
20E2A-3-A6-IR	PRAPRSFYDAIHQLVGRQPGG	17.8	19.1	7.6	2.5
20E2A-4-G12-IR	PCSDDQFYDALSQLVGIRVCP	9.0	9.3	2.6	3.6
	SYGYQSFYDAIEELVRGPPAR				0.3

FIGURE 2L (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
D sign		E-Tag	IGFsR	IR	IGF/IR	IR/IGF
Parental	XXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-4-F11-IGFR	FYDAIDQLVGRSARAGGTRD	30.6	15.1	4.2	3.6	0.3
20E2A-4-F12-IGFR	QGSASFYDAIDRLRLMRIGG	21.3	18.8	1.3	14.6	0.1
20E2A-3-B4-IGFR	AQSGEGFYDALAQVLVQGVSG	23.3	23.9	3.1	7.8	0.1
20E2A-4-F4-IGFR	GHPAVSFYDAIDQLLRRRGGG	21.8	16.6	2.4	6.9	0.1
20E2A-3-C7-IGFR	YSDTYSFYDAIVQLVRRGASA	20.7	20.0	3.6	5.5	0.2
20E2A-3-C10-IGFR	VGTVAGFYDAIAQLVARASRV	17.6	5.4	1.1	5.1	0.2
20E2A-3-D6-IGFR	RFVWGSFYDAIDQLVQGRWRG	23.3	21.0	4.2	5.0	0.2
20E2A-4-F6-IGFR	RAVGDSFYEAIDQLVRRGGHV	15.1	11.8	2.4	5.0	0.2
20E2A-3-A8-IGFR	LRSQLSFYEAIDQLVQWKGGA	21.5	19.9	4.3	4.6	0.2
20E2A-4-F9-IGFR	DKFTTSFYDAIDQLVQSVRGV	22.2	13.3	2.9	4.6	0.2
20E2A-4-F3-IGFR	MQSGFSFYDAIDRLVGRGLGER	21.2	19.0	4.4	4.4	0.2
20E2A-3-B2-IGFR	VGSSSFYEAIERLVQGLGRH	20.6	19.3	4.6	4.2	0.2
20E2A-4-G8-IGFR	LSWAAGFYEAIDQLVRSGGHR	18.7	14.7	3.8	3.9	0.3
20E2A-3-D10-IGFR	QQVHAGFYEAIEELVGFGLG	20.9	10.8	2.7	3.9	0.3
20E2A-3-A12-IGFR	MMVVDGFYDALHQLVVAQSLG	20.6	6.9	1.8	3.9	0.3
20E2A-3-A11-IGFR	LSVALSFYDALGQLVAGEGRW	16.1	4.3	1.1	3.9	0.3
20E2A-4-H1-IGFR	SGSNLGFYDALRQLVGATDGS	17.8	9.7	2.6	3.7	0.3
20E2A-4-F7-IGFR	PSGFLSFYEAIDQLVHGVRWF	20.8	14.5	4.1	3.5	0.3
20E2A-3-D7-IGFR	AFTPTSFYDAIEQLVQQLSPR	19.5	17.9	5.3	3.4	0.3
20E2A-3-A9-IGFR	VSSLRSFYDALDELVRRPFQ	22.0	18.3	5.6	3.3	0.3
20E2A-3-A10-IGFR	VSMPPSFYDALKQLVRGISEG	24.7	10.5	3.2	3.3	0.3
20E2A-3-B11-IGFR	IGVSRGFYDAIDKLVRDRGSP	26.3	15.4	4.8	3.2	0.3
20E2A-3-D12-IGFR	GRSLLSFYDLIDQLVQAGNGG	15.8	10.7	3.4	3.2	0.3
20E2A-4-H11-IGFR	GQRAQSFYEAIALRLVCEGRCT	13.9	9.0	2.8	3.2	0.3
20E2A-4-H5-IGFR	CRFQGSFYDAIDLLVLGVRTC	22.8	17.5	5.7	3.1	0.3
20E2A-4-E11-IGFR	RWAFQSFYDAIDHLVNHREGH	20.1	16.6	5.5	3.0	0.3
	LPSSSGFYNAIQQLVCGHRGC	21.0	12.6	4.2	3.0	0.3

FIGURE 2M

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-4-F2-IGFR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-3-D4-IGFR	TGVFNDFYDALQQLVGRVRD	19.4	19.0	6.8	2.8	0.4
20E2A-3-B10-IGFR	YGSFETFYDAIDQLVRRGSQP	16.1	11.8	4.2	2.8	0.4
20E2A-4-E5-IGFR	RQLLDSFYEAIDQLVRSERP	24.0	14.3	5.3	2.7	0.4
20E2A-3-D5-IGFR	WPRGDPFYDAMEKLLSQGGGR	18.1	20.6	7.9	2.6	0.4
20E2A-4-G11-IGFR	PGLIQSFYDAIDQLVQRGRN	15.1	9.3	3.6	2.6	0.4
20E2A-3-C12-IGFR	MNVFVSFYDAIDQLVCQIGC	20.7	3.3	1.3	2.6	0.4
20E2A-4-G5-IGFR	LDMIGGFYEAIDQLVSGSLAP	25.9	17.4	7.2	2.4	0.4
20E2A-3-D9-IGFR	RRPCNSFYDAIQQLLVGGPCG	23.6	14.6	6.0	2.4	0.4
20E2A-4-F10-IGFR	FGRRSTFYDLIDQLVGQGRGT	19.8	12.3	5.1	2.4	0.4
20E2A-4-E2-IGFR	LRAPRSFYEAIYQLAQRPSVP	21.4	21.6	9.3	2.3	0.4
20E2A-4-E3-IGFR	VQRFSSFYDALDQLVGHGVWK	22.6	21.3	9.1	2.3	0.4
20E2A-3-C4-IGFR	PSARMGFYDLIDQLVGLVPGS	21.0	21.8	10.1	2.2	0.5
20E2A-3-C5-IGFR	SLQPHDFYDAIHRLVFHGGRF	23.5	17.4	7.8	2.2	0.4
20E2A-4-G12-IGFR	ERHGSFYDAIAQLLQSDRSR	22.2	17.1	7.7	2.2	0.4
20E2A-3-C3-IGFR	YQPPGSFYDWIRELVAGPRRE	24.3	16.3	7.4	2.2	0.5
20E2A-4-E10-IGFR	FAHASSFYDAIDQLVAKCQSP	11.3	2.7	1.2	2.2	0.5
20E2A-4-E6-IGFR	AQSSSGFYEALYQLVWGRPG	22.3	22.6	10.8	2.1	0.5
20E2A-3-B7-IGFR	TTSGGSFYDAMYQLVWGDWRR	22.6	19.9	9.4	2.1	0.5
20E2A-4-D3-IGFR	ARGTAGFYAELERLVRGQDHG	23.0	16.6	7.9	2.1	0.5
20E2A-4-G4-IGFR	PRHAINFYDAIHQLVFGPRQ	20.5	15.7	7.6	2.1	0.5
20E2A-4-F1-IGFR	QSAHWSFYDAIERLVNMDTMP	22.6	14.5	7.0	2.1	0.5
20E2A-4-H7-IGFR	VGVVSSFYDAIDQLVWDRGS	19.6	19.9	9.8	2.0	0.5
20E2A-3-B9-IGFR	DTLIASFYDAIDQLVRLGRNQ	23.0	17.1	8.7	2.0	0.5
20E2A-4-E9-IGFR	FQGTQGFYDAIERLMRRGERP	26.4	22.1	11.5	1.9	0.5
20E2A-3-B1-IGFR	WADWGSFYDAIEQLVQRGGGV	25.3	20.7	11.1	1.9	0.5
20E2A-4-G1-IGFR	EQLSCGFYDAIHQLVHGGGLG	23.1	17.9	9.5	1.9	0.5
20E2A-4-E7-IGFR	CGQRCSFYDAIDQLVGLPGA	22.6	17.7	9.3	1.9	0.5
20E2A-3-D11-IGFR	MMRVDFGYEAIIDRLVNEGQAT	17.2	8.6	4.6	1.9	0.5
20E2A-3-A3-IGFR	RQATSFYEAIDQLMGSGGV	16.1	6.1	3.2	1.9	0.5
20E2A-4-G7-IGFR	GHYFGSFYDAIDQLVAGMLPG	5.2	3.0	1.5	1.9	0.5
	PEGVQGFYDALAHLVGGSLFG	24.4	21.1	11.5	1.8	0.5

FIGURE 2M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-4-G2-IGFR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-4-G3-IGFR	IGVLGSFYDAIDQLVRQGNR	22.3	17.5	9.9	1.8	0.6
20E2A-3-B5-IGFR	RDVADGFYAAIEQLVRGQGL	21.2	12.3	6.9	1.8	0.6
20E2A-4-H4-IGFR	VRQAKSFYDAIDQLVRGALRG	24.0	22.7	13.3	1.7	0.6
20E2A-4-F8-IGFR	QVFRGSFYDAIDALVRWGGR	22.2	20.6	12.0	1.7	0.6
20E2A-3-A6-IGFR	VGAASFYDAIDQLVGSWSPGS	17.3	17.9	10.7	1.7	0.6
20E2A-4-H12-IGFR	PSPVWSFYDAIQQLVRSQGRG	23.8	23.7	15.0	1.6	0.6
20E2A-3-B12-IGFR	PVSATSFYDAINQLVRMCSRG	25.1	23.5	14.2	1.6	0.6
20E2A-3-B8-IGFR	VMRRDRFYDAIEQLVGGRIQV	27.6	21.9	13.6	1.6	0.6
20E2A-3-C8-IGFR	TTYVNSFYDALQQLLGGDADV	21.5	19.0	12.2	1.6	0.6
20E2A-4-H10-IGFR	LSNMITFYDAINQLVGHVQSL	23.2	17.7	11.4	1.6	0.6
20E2A-3-C9-IGFR	ASSRLSFYDAIEQLIKWSPGP	25.3	23.8	16.2	1.5	0.7
20E2A-4-H2-IGFR	WDLVDSFYDAIDQLVGQVRPG	25.4	21.8	14.6	1.5	0.7
20E2A-3-B6-IGFR	FAFVGSFYDALAQLVAQGPRS	21.8	20.1	13.0	1.5	0.6
20E2A-4-G9-IGFR	EDQPNFSFYDAIRQLVMGRLSP	20.3	18.1	11.8	1.5	0.7
20E2A-4-H6-IGFR	SVGPRSFYDAIDQLVGGAWVG	26.0	16.1	10.8	1.5	0.7
20E2A-4-G10-IGFR	KFRVYTFYDAIDQLVNQGRGR	21.9	19.6	13.9	1.4	0.7
20E2A-3-A4-IGFR	GRGWGSFYEAIDQLVRGLGET	24.9	16.8	11.8	1.4	0.7
20E2A-3-A7-IGFR	FTSFHTFYDAIEQLVQGQGGDP	25.3	16.5	12.1	1.4	0.7
20E2A-4-E12-IGFR	AGSVTSFYDAMEQLVATG TSA	16.8	2.5	1.8	1.4	0.7
20E2A-3-D1-IGFR	PRESFSFYDAIHQLVTGRVRS	26.0	24.9	19.3	1.3	0.8
20E2A-3-C6-IGFR	LGRADGFYDAIKQLVGADWGG	23.3	23.1	17.8	1.3	0.8
20E2A-3-D2-IGFR	RSGTWTFYDALELLVQSGSR	24.0	22.4	17.6	1.3	0.8
20E2A-4-E8-IGFR	PVWLFSFYDAIDQLVRKGLGP	23.7	21.7	17.2	1.3	0.8
20E2A-4-G6-IGFR	GRRRQTFYDALEQLVGGGALG	21.4	15.1	11.4	1.3	0.8
20E2A-4-F5-IGFR	AGPDMSFYDAIDQLVHCCGPF	18.4	13.6	10.4	1.3	0.8
20E2A-3-C2-IGFR	HGEKLSFYDAIAQLVGFIDIGH	24.7	21.9	17.7	1.2	0.8
20E2A-4-H8-IGFR	GYTPVDFYDAIRQLVTGWPG	21.7	21.7	18.2	1.2	0.8
20E2A-3-A5-IGFR	FGGFSSFYDALDQLARGGSD	22.5	19.6	15.8	1.2	0.8
20E2A-3-C11-IGFR	VGIVRGFYEAIERLVGDTHGQ	24.4	18.5	15.1	1.2	0.8
	TPGGFSFYDAIQQLVDVLSDS	22.7	15.6	12.6	1.2	0.8
	TNAALTFYDAIEQLVRWGQRD	25.8	24.3	21.2	1.1	0.9

FIGURE 2M (Con't)

20E2A-3-C1-IGFR

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-3-C1-IGFR	XXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-3-B3-IGFR	GQSPLSFYDAIDQLVRAFPVG	23.4	22.4	20.5	1.1	0.9
20E2A-3-D8-IGFR	AGQLGGFYIAICQLVGYEYCT	21.0	17.0	14.8	1.1	0.9
	SAGPLSFYDAIAQLVGPWRL	22.0	19.7	19.6	1.0	1.0

FIGURE 2M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXFYXXhxxhXXXXXXXX FYDAIDQLVRGSARAGGTRD	--	--	--	--	--
20E2Bα-3-B3-IR	AGVNAGFYRYFSTLLDWDQ	30.6	15.1	4.2	3.6	0.3
20E2Bα-4-F12-IR	SVKEVQFYRYFYDLLQSESG	33.5	1.2	23.5	0.1	20.0
20E2Bα-3-B8-IR	IEVTQPFYDYFQQLRLRYGND	35.5	5.9	27.8	0.2	4.7
20E2Bα-3-D2-IR	VQCRADFYSYFACLVGRPGSR	39.3	18.2	36.5	0.5	2.0
20E2Bα-3-A5-IR	RNYPIGFYQFFHELVISSGG	42.6	19.7	26.7	0.7	1.4
20E2Bα-3-A3-IR	DLGNSFYGLRLRLVLQDAVG	36.9	22.7	24.5	0.9	1.1
20E2Bα-4-E9-IR	CKDQPDFYMGIKCLISGGSV	39.9	33.5	35.5	0.9	1.1
20E2Bα-4-G8-IR	ACEGGSFYGCLQSLMSVESGN	32.8	29.6	28.6	1.0	1.0
20E2Bα-4-F9-IR	AVHEDGFYDMLRKLLSEGDS	37.5	30.5	30.9	1.0	1.0
20E2Bα-4-E7-IR	LARDEFYRYFEQLVFGDTG	35.6	32.5	31.1	1.0	1.0
20E2Bα-3-D5-IR	ATCASSFYAQLNCLLSDFDVM	36.0	31.6	31.2	1.0	1.0
20E2Bα-4-F7-IR	VQACQNFYDCINTLLLLDLGG	39.5	33.1	31.8	1.0	1.0
20E2Bα-3-B12-IR	IRGADQFYQFFRELLEGVGE	36.6	32.9	32.5	1.0	1.0
20E2Bα-3-A11-IR	RAGSRGFYEFFENLLRVGAGG	37.0	33.4	33.5	1.0	1.0
20E2Bα-3-B7-IR	AQRCADFYACIEELLAPGSR	36.9	34.9	34.2	1.0	1.0
20E2Bα-3-B5-IR	PGGEGFYQGLQRLILGADGG	40.4	37.1	36.3	1.0	1.0
20E2Bα-4-G1-IR	QKRSEAFYDWIADLLGQETSG	41.6	36.4	34.5	1.1	1.0
20E2Bα-4-G11-IR	WGLRDDFYRGIRCLVQWSEGC	38.5	28.9	26.5	1.1	0.9
20E2Bα-4-E10-IR	DSTVCGFYCRLAQLVAEGGSP	33.2	30.1	27.8	1.1	0.9
20E2Bα-4-F11-IR	QHSCRTFYDCIRVLMDDGQLG	35.4	30.5	28.0	1.1	0.9
20E2Bα-4-H11-IR	WSGNVDFYMYIRQLCGDVCS	32.5	29.5	28.0	1.1	0.9
20E2Bα-4-H3-IR	QTVHRDFYAALQDLLINDLGF	34.8	32.0	28.7	1.1	0.9
20E2Bα-4-H7-IR	SSGCQDFYSCMIQLVTTGGGD	38.7	34.9	30.5	1.1	0.9
		35.3	32.5	30.5	1.1	0.9

FIGURE 2N

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2Bα-3-B6-IR	SGPMVGFYRGLFSLSPEDLQ	39.7	34.9	31.5	1.1	0.9
20E2Bα-3-D1-IR	LAEPDSFYNWIQALLEEFAG	41.6	35.1	31.7	1.1	0.9
20E2Bα-3-A9-IR	FSGCDNFYSCIQSLWLPGGV	37.3	35.1	32.4	1.1	0.9
20E2Bα-3-C4-IR	QVFCDNFYHCIEIETLLGVQTP	39.6	36.3	33.4	1.1	0.9
20E2Bα-4-F3-IR	RGRDNQFYHGLWALLGSGLE	37.5	36.6	33.6	1.1	0.9
20E2Bα-4-F4-IR	VSGRGGFYDAIRDLIIPRDQG	37.2	36.9	33.7	1.1	0.9
20E2Bα-3-D4-IR	PVVLDDEFYVALCQLMVQGDCF	42.1	38.0	34.5	1.1	0.9
20E2Bα-4-E4-IR	PDIADPFYAFFQGLLRADTPI	40.6	38.4	35.5	1.1	0.9
20E2Bα-4-G10-IR	VAQCTDFYACIRSLVRSGPSG	32.9	31.3	27.1	1.2	0.9
20E2Bα-3-D11-IR	CSQLVSFYLGMDCLLGRGGTQ	34.0	32.5	27.9	1.2	0.9
20E2Bα-3-C8-IR	PLACADFYQCLSDLIRGGPAW	39.2	33.0	28.2	1.2	0.9
20E2Bα-4-F2-IR	VVICTFGYDCIYQLVGSHEEM	38.7	37.6	32.3	1.2	0.9
20E2Bα-4-H12-IR	CVDRRTFYEGLQCLLGATGD	32.3	30.4	25.8	1.2	0.8
20E2Bα-4-E1-IR	VNLRDPFYQWIEALMDSAGGE	39.2	40.2	32.3	1.2	0.8
20E2Bα-4-H8-IR	LTSSTSFYDALFCLAGLQCG	37.6	34.8	27.0	1.3	0.8
20E2Bα-3-B4-IR	DFDSSPFYRGLRQLLESRSFP	39.9	34.9	25.9	1.3	0.7
20E2Bα-4-E2-IR	HEAGWTFYDAIQCLVGGWCSK	38.8	36.3	23.5	1.5	0.6
20E2Bα-4-H1-IR	CQQWRSFYHAVSCLLGPDPD	40.8	33.6	20.2	1.7	0.6
20E2Bα-3-A10-IR	MVDRDPFYQGLRDLIGRQEKG	32.8	32.6	18.5	1.8	0.6
20E2Bα-3-D3-IR	LGRRGGFYRGLQDLIGTOWPR	41.9	29.5	5.6	5.3	0.2

FIGURE 2N (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
20E2Bβ-4-F7-IR	DALNLFYSYFQHLMEDQVTD	26.8	3.0	24.2	0.1	8.0
20E2Bβ-3-E12-IR	GNSGGSFYRYFQLLLDSDGMS	17.2	1.4	5.5	0.3	4.0
20E2Bβ-4-F3-IR	GDRVPGFYDWIRQLMVDPLEV	25.2	2.0	7.7	0.3	3.9
20E2Bβ-4-F6-IR	SEREDPFYRWIQAMVEGVSEG	25.7	3.8	11.0	0.4	2.9
20E2Bβ-3-D11-IR	GSVACDFYCHMWSLVEQPAGT	14.8	3.6	4.2	0.9	1.2
20E2Bβ-3-E5-IR	VHPSAGFYKGLLALIGDSQLG	24.3	6.9	4.3	1.6	0.6
20E2Bβ-3-C9-IR	FCGGLSFYGCQLQELLTWESPT	29.7	24.3	15.0	1.6	0.6
20E2Bβ-3-C7-IR	QSGSGDFYDWLSRLIRNGDGG	1.5	3.1	1.5	2.0	0.5
20E2Bβ-4-H8-IR	LPRQDGFYDALRRLISEGAGG	25.8	26.9	13.2	2.0	0.5
20E2Bβ-4-G7-IR	LQPCSGFYECIERLIGVKLSG	19.9	25.2	1.6	15.8	0.1

FIGURE 2N (Con't)

Clone	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	--
Design	XXXXXXXXXXXXXXXXXXXX	--	----	--	--	--	--
20E2B-1-A6-IGFR	GVRAMSFYDALVSVLGLPSG	18.6	18.1	1.1	16.8	0.1	1.1
20E2B-3-C6-IGFR	VEGRGLFYDLLRQLLARRQNG	17.9	16.8	1.1	14.8	0.1	1.1
20E2B-4-H3-IGFR	KLHNLMPFYGLQRLVWGAGLG	11.2	14.8	1.1	13.9	0.1	1.1
20E2B-3-C2-IGFR	GNGDGMFYQLLSLLVGRDMHV	13.1	8.9	0.6	13.8	0.1	1.1
20E2B-3-E3-IGFR	PDLHKGFYAQLAIRGQLLS	22.4	16.3	1.3	13.1	0.1	1.1
20E2B-4-H12-IGFR	YSCGDGFYSLLSDLLGGQFRC	6.5	9.7	0.8	12.8	0.1	1.1
20E2B-3-D2-IGFR	IQQLTFYDLLHRLVRSELGS	20.7	12.4	1.1	11.7	0.1	1.1
20E2B-3-D8-IGFR	GGTEVDFYRALERLVRGQLGL	20.4	17.7	1.6	11.3	0.1	1.1
20E2B-3-E8-IGFR	LRIANLFYQRLWDLAFGGGG	15.7	16.7	1.5	11.1	0.1	1.1
20E2B-4-F8-IGFR	PVGVGQFYEGLSRLVLGRGW	12.3	7.3	0.8	9.7	0.1	1.1
20E2B-1-A11-IGFR	RFSTDGFYQYLLALVGGPVG	15.0	9.5	1.0	9.7	0.1	1.1
20E2B-3-D4-IGFR	NSRDGGFYQLERLLGFPVTG	8.1	7.9	0.8	9.6	0.1	1.1
20E2B-2-B11-IGFR	VVTPVNFYRALEALVRGQRLG	13.9	10.6	1.1	9.4	0.1	1.1
20E2B-3-C8-IGFR	QPAPDGFYSALMKLIGRGVS	18.5	15.6	1.8	8.9	0.1	1.1
20E2B-2-B2-IGFR	PGTDLGFYQALRCVVIQACD	11.7	4.9	0.6	8.1	0.1	1.1
20E2B-4-F10-IGFR	AQPCGGFYGLLEQLVGRSVCD	19.0	17.3	2.2	7.8	0.1	1.1
20E2B-4-F9-IGFR	QPDHSFYFYSLLQELVGSEERL	11.9	14.7	1.9	7.7	0.1	1.1
20E2B-3-D11-IGFR	LGVTDGFYAALGYLIHVGQF	14.3	12.2	1.6	7.6	0.1	1.1
20E2B-3-C11-IGFR	CMMQDGFYAGLGCLLTAGEGR	15.3	15.4	2.1	7.5	0.1	1.1
20E2B-2-B3-IGFR	ICTGGGFYQVLCGLLRGTSAR	9.1	5.3	0.7	7.4	0.1	1.1
20E2B-3-D12-IGFR	QGNVLDFFYGWIGRLLAKQGS	10.3	6.2	0.9	7.3	0.1	1.1
20E2B-3-E12-IGFR	VATSQGFYSGLSELQGGGNV	13.9	6.0	0.8	7.3	0.1	1.1
20E2B-2-B8-IGFR	IWATGDFYRLLSQLVMGRVGT	17.4	5.7	0.8	7.2	0.1	1.1
20E2B-4-G11-IGFR	RQGTGSFYLMLEQLLVGARGP	8.9	4.5	0.6	7.0	0.1	1.1
20E2B-3-D6-IGFR	DSVGDNFYQLLESLVGGHVG	20.7	17.8	2.6	6.9	0.1	1.1
20E2B-2-B7-IGFR	LSSDQGFYRALNLLLQGSAGR	18.0	6.1	0.9	6.7	0.1	1.1
20E2B-3-C4-IGFR	ASSASGFYELLQRLAGLGLV	23.4	20.4	3.3	6.2	0.2	1.1

FIGURE 20

Clone	Sequence	Randomized Sequences				Comparisons			
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	IGFR/IR	IR/IGFR	
Design	XXXXXXXXFYXXhXXXXXXXX	--	--	--	--	--	--	--	
20E2B-3-D3-IGFR	CGRRDFYGGIICLLGQKGVV	21.0	16.1	2.6	6.2	6.2	0.2	0.2	
20E2B-4-H8-IGFR	PAGPCGYCGLGLLLHGDQSP	7.2	5.3	0.9	5.9	5.9	0.2	0.2	
20E2B-3-E9-IGFR	QAAPQDFYQGLWLLIHRDPTM	14.7	16.2	2.8	5.8	5.8	0.2	0.2	
20E2B-4-H9-IGFR	RCQGTGFYTCIQELIGFGDPD	4.5	5.2	0.9	5.6	5.6	0.2	0.2	
20E2B-1-A8-IGFR	TLRSPTFYDWLEMLVTHGQGG	16.1	4.4	0.9	5.0	5.0	0.2	0.2	
20E2B-4-H11-IGFR	STHSAFYDAIAQLVGSVLGP	10.7	11.0	2.3	4.8	4.8	0.2	0.2	
20E2B-3-C9-IGFR	RQGGSFYELLCGLVGGEVCV	17.9	19.7	4.2	4.6	4.6	0.2	0.2	
20E2B-3-E6-IGFR	RQASGFYRALHDLMLRTQDY	24.5	21.6	4.7	4.6	4.6	0.2	0.2	
20E2B-3-E11-IGFR	SRNNLFYMGLSQLLRNRL	16.5	7.7	1.9	4.1	4.1	0.2	0.2	
20E2B-4-G8-IGFR	GRALDPFYDQLRDLVARSGG	11.1	14.9	3.7	4.1	4.1	0.2	0.2	
20E2B-4-H10-IGFR	EASCRTFYCGLMALIGDDQR	2.2	2.5	0.8	3.1	3.1	0.3	0.3	
20E2B-3-E7-IGFR	QNGCKDFYCLIDNLIRYPGG	14.4	8.8	3.0	3.0	3.0	0.3	0.3	
20E2B-3-C12-IGFR	QHSCRTFYDCIRVLMDDGQLG	6.2	6.4	2.2	2.9	2.9	0.3	0.3	
20E2B-4-G12-IGFR	LDSRRGFYDWIKALIGDRDVQ	9.6	10.0	3.8	2.6	2.6	0.4	0.4	
20E2B-4-G3-IGFR	CQKKGDFYAGLVCLLRERASQ	27.2	23.8	9.1	2.6	2.6	0.4	0.4	
20E2B-3-E4-IGFR	GGSQSFYDVMCMLLQLDPTC	24.9	22.3	8.9	2.5	2.5	0.4	0.4	
20E2B-3-E2-IGFR	VESDVSFYEGLMRLVWVGQGG	18.6	20.2	8.7	2.3	2.3	0.4	0.4	
20E2B-2-B4-IGFR	ERAGDLFYQWFERLVAGHGLE	5.8	2.3	1.0	2.2	2.2	0.5	0.5	
20E2B-3-C5-IGFR	RMPSGSFYQGIYELVTRQGGF	6.3	2.0	0.9	2.2	2.2	0.5	0.5	

FIGURE 20 (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXFYRYFXXLLXXXXXX	--	--	--	--	--
NMRPβ-4-G6-IR	RWPNFYGYFESLLTHFS	10.1	1.9	20.1	0.1	10.6
NMRPβ-4-F3-IR	HYNAFYEFYFQVLLAETW	8.6	1.3	13.6	0.1	10.5
NMRPα-2-C1-IR	EGWDFYSYFSGLLASVT	19.7	2.0	10.9	0.2	5.3
NMRPα-4-E1-IR	LDRQFYRYFQDLLVGFM	11.5	6.5	21.2	0.3	3.2
NMRPα-3-H6-IR	WGRSFYRYFETLLAQGI	19.1	2.1	6.0	0.3	2.9
NMRPβ-4-F7-IR	RREGFYHYFQSLLEYG	0.7	0.9	2.3	0.4	2.7
NMRPα-2-D1-IR	GGGQFYRYFIDMLVLDI	18.4	1.5	3.7	0.4	2.5
NMRPα-1-A1-IR	PTGPFDRYFARRLVWRG	15.2	1.3	3.1	0.4	2.4
NMRPα-2-C10-IR	RGGAFYRYFEGLLSQHN	18.8	3.8	8.8	0.4	2.3
NMRPα-3-G1-IR	WRDPFYRYFQDLLLEGER	18.9	4.2	8.6	0.5	2.1
NMRPα-4-C3-IR	WGGEFYRYFVQLLSSD	17.9	12.9	25.7	0.5	2.0
NMRPα-4-D1-IR	GRESFYGYFLDLLQETV	16.2	12.7	23.2	0.5	1.8
NMRPβ-4-F4-IR	GHAEFYGYFQGLLDSYL	19.5	16.0	25.6	0.6	1.6
NMRPα-1-B2-IR	GGEAFYRYFWGLLTEWE	14.8	8.4	12.9	0.7	1.5
NMRPα-1-B4-IR	LSSGFYRYFTGLLSDGQ	19.1	6.3	9.2	0.7	1.5
NMRPα-4-D9-IR	DPGAFYRYFAQLMDTWN	7.6	16.9	25.7	0.7	1.5
NMRPβ-4-F2-IR	KHEQFYVEYFRNLLGAMS	21.6	20.9	30.8	0.7	1.5
NMRPβ-4-H12-IR	RDGAFYRYFEDLLIAVD	5.2	13.8	20.0	0.7	1.5
NMRPα-4-E7-IR	RGNRFYEFYELLRDYG	9.4	21.9	29.7	0.7	1.4
NMRPα-1-B5-IR	ELGDFYRYFQLLLADWH	14.1	5.4	7.1	0.8	1.3
NMRPα-4-C4-IR	AQDAFYSYFSVLLGEHL	17.6	17.6	22.3	0.8	1.3
NMRPα-4-C7-IR	IGVNFYRYFEKLLLDDEF	4.5	11.2	14.9	0.8	1.3
NMRPα-4-D3-IR	TDSQFYSYFESLLETFG	16.4	13.5	17.9	0.8	1.3

FIGURE 2P

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXFYRYFXXLLXXXXXXXX	--	--	--	--	--
NNRPβ-4-G10-IR	SSREFSYFSGLLTAL	8.8	8.7	11.7	0.7	1.3
NNRPβ-4-H2-IR	TGRGFYRYFEGLLDWM	4.9	19.9	25.3	0.8	1.3
NNRPa-4-C1-IR	SGSWFYRYFEEELLQSG	15.5	18.0	21.1	0.9	1.2
NNRPa-4-C5-IR	GRGGFYQYFLDLLQTEA	18.0	23.3	26.9	0.9	1.2
NNRPa-4-C6-IR	GQNGFYRYFDTLLADWV	7.8	13.6	15.7	0.9	1.2
NNRPa-4-C12-IR	FAGSFYRYFEQLLSEQ	12.3	16.7	19.9	0.8	1.2
NNRPa-4-D7-IR	DPNAFYRYFEGLLWREH	10.2	23.7	27.9	0.8	1.2
NNRPa-4-D11-IR	?GLNFYRYFVGLLTDTL	5.4	19.3	22.3	0.9	1.2
NNRPβ-4-F1-IR	RHINFYGYFDDLLATWH	21.7	23.0	28.6	0.8	1.2
NNRPβ-4-F9-IR	FHRGFYRYFINLLSGDA	10.1	18.4	22.5	0.8	1.2
NNRPβ-4-F12-IR	MGSSFYRYFETLLGQGL	4.5	13.5	16.6	0.8	1.2
NNRPy-4-A3-IR	GSLDFYSYFWERLGLGP	16.4	22.3	26.8	0.8	1.2
NNRPa-1-A7-IR	STVSFYRYFYALLQSPC	16.9	1.2	1.3	0.9	1.1
NNRPa-4-C11-IR	LGGYFYRYFEDLLNHQS	7.8	19.7	21.2	0.9	1.1
NNRPa-4-D8-IR	DHRGFYRYFLYQLAGNV	6.9	17.6	20.1	0.9	1.1
NNRPa-4-D10-IR	EYSGFYGYFNHLLGSLG	6.4	17.2	19.5	0.9	1.1
NNRPa-4-E5-IR	TSNWFYQYFTDLLAGED	13.2	26.1	27.6	0.9	1.1
NNRPa-4-E8-IR	SSGGFYRYFSQLLTEMN	8.7	22.9	24.2	0.9	1.1
NNRPa-4-E10-IR	VHGEFYRYFESLLRETF	3.5	12.4	13.2	0.9	1.1
NNRPβ-4-F8-IR	SDEGFYRYFAQLLYGVT	8.1	22.9	25.2	0.9	1.1
NNRPβ-4-F10-IR	ETGGFYGYFQALLATYH	5.3	17.9	19.1	0.9	1.1
NNRPβ-4-G8-IR	GDRGFYRYFEWLLNDFG	10.6	27.2	28.9	0.9	1.1
NNRPβ-4-H3-IR	FGGAFYRYFEALLGEMG	3.9	24.2	25.7	0.9	1.1
NNRPβ-4-H9-IR	DGGAFYRYFEALLGELD	4.1	26.5	29.3	0.9	1.1
NNRPβ-4-H10-IR	WHSDFYRYFLSLLQEDG	3.4	22.3	24.6	0.9	1.1
NNRPy-4-A6-IR	EEEGFYGYFYRLLGVER	14.9	25.8	27.6	0.9	1.1
NNRPy-4-A8-IR	MDAGFYGYFSDLLANWG	9.8	22.8	24.7	0.9	1.1

FIGURE 2P (Con't)

Clone Design	Sequence XXXXXXXXFYRYFXXLLXXXXXXXX	E-Tag --	ICFR --	IR --	ICFR/IR --	IR/ICFR --
NNRPγ-4-A10-IR	SGFAFYQYFQELLAGHD	7.6	20.3	22.0	0.9	1.1
NNRPγ-4-B6-IR	GDGGFYGYFASLLSGEG	12.2	22.3	24.2	0.9	1.1
NNRPγ-4-B9-IR	EANGFYRYFYDLLQDFG	6.7	22.9	25.9	0.9	1.1
NNRPα-4-C8-IR	AVNGFYRYFNRLLESVE	8.5	16.3	16.0	1.0	1.0
NNRPα-4-C9-IR	QQDGFYRYFLDLLDEVA	5.6	20.7	19.9	1.0	1.0
NNRPα-4-C10-IR	ISQGFYGYFSRLLQDTE	6.7	16.5	17.2	1.0	1.0
NNRPα-4-E11-IR	YSTGFYRYFLDLLDGMP	6.0	20.3	20.9	1.0	1.0
NNRPβ-4-F11-IR	PNGDFYRYFLDLLGSVG	7.7	21.8	21.9	1.0	1.0
NNRPβ-4-G2-IR	RHQAFYSYFRDLPREC	19.1	24.7	25.6	1.0	1.0
NNRPβ-4-G9-IR	ETEGFYRYFEELLAQVA	7.8	27.3	26.4	1.0	1.0
NNRPβ-4-H7-IR	AGDRFYDYFDRLLADYD	2.6	26.6	27.9	1.0	1.0
NNRPβ-4-H8-IR	GGSGFYRYFWGLLAEQE	3.6	23.0	24.1	1.0	1.0
NNRPγ-4-B1-IR	LLNRLYRYFAGAEWFG	17.6	24.5	23.4	1.0	1.0
NNRPγ-4-B10-IR	DGSGFYRYFEMLLGSGL	5.5	18.3	19.0	1.0	1.0
NNRPα-1-B3-IR	RDMAFYRYFSHLLLESFQ	16.4	13.4	12.7	1.1	0.9
NNRPα-2-C2-IR	GNAGFYRISRILWQGT	22.5	24.4	21.3	1.1	0.9
NNRPα-2-C3-IR	GNAGFYRYFADLMAGYE	19.6	21.7	19.7	1.1	0.9
NNRPα-2-D10-IR	YQAAFYRYFATLLSTTD	17.8	6.3	5.4	1.2	0.9
NNRPα-3-E11-IR	GGLGFYRYFQLLLGSSG	12.9	10.8	9.6	1.1	0.9
NNRPα-3-F5-IR	DGSGFYGYFDFVLRQFE	25.1	18.3	17.0	1.1	0.9
NNRPα-3-F8-IR	VGSGFYRYFDQLLGMYG	22.2	15.7	13.9	1.1	0.9
NNRPα-3-F10-IR	YGTDFYLYFDQLLLQYG	20.5	14.6	13.1	1.1	0.9
NNRPα-3-G7-IR	FNSSFYLYFRDLLNTVG	21.0	18.3	15.6	1.2	0.9
NNRPα-4-C2-IR	RAAGFYRYFEDLLGARG	25.5	25.1	23.3	1.1	0.9
NNRPα-4-D12-IR	TGAGFYRYFIDLGETG	14.7	19.7	18.5	1.1	0.9
NNRPβ-4-G3-IR	RDLEFYGYFQELLRLNF	14.6	27.8	25.7	1.1	0.9
NNRPβ-4-G4-IR	GMGPFYRYFIDLLRES	20.0	28.6	24.9	1.1	0.9
NNRPγ-4-A5-IR	HGDGFYQYFMEVLRQN	17.0	29.0	27.3	1.1	0.9

FIGURE 2P (Con't)

Clone Design	Sequence	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
NNRPβ-4-H11-IR	XXXXXXXXFYRYFXLLXXXXXXXX	--	--	--	--	--
NNRPα-1-B1-IR	DYTA FYGYFNNLLRTSG	2.3	12.4	9.0	1.4	0.7
NNRPα-2-D7-IR	FQSSFYGYFESLLMSYK	18.8	18.7	11.5	1.6	0.6
NNRPα-2-D8-IR	DTNA FYRYFEGLLWSEH	21.0	21.8	13.2	1.6	0.6
NNRPα-3-E1-IR	GGSSFYRYFEQLLAQWE	20.2	19.8	12.2	1.6	0.6
NNRPα-3-E5-IR	SQGGFYRYFEKLLDEVT	20.0	20.5	12.9	1.6	0.6
NNRPα-3-H3-IR	RSGLFYRYFEELLQGA I	20.0	24.5	15.5	1.6	0.6
NNRPα-3-H5-IR	QGGFYHYFLSLLLEV G	19.8	19.1	12.2	1.6	0.6
NNRPα-1-A3-IR	WRGA FYRYFQTLSD EG	19.9	18.0	11.1	1.6	0.6
NNRPα-3-E6-IR	AAGFYGYFYSLLGDQT	24.4	14.9	7.9	1.9	0.5
NNRPα-3-F9-IR	RNSGFYRYFQHLVSEWE	23.1	19.0	9.6	2.0	0.5
NNRPα-3-G6-IR	QHRLFYSYFAELLGRDT	21.1	18.8	9.6	1.9	0.5
NNRPα-3-H9-IR	QIDEFYRYFADQLRGFA	22.4	17.7	9.0	2.0	0.5
NNRPα-1-A8-IR	LGGFYRYFNLLVMGSG	18.3	13.1	6.9	1.9	0.5
NNRPα-1-A9-IR	GDRA FYRYFQRQLEGWG	16.9	13.8	5.7	2.4	0.4
NNRPα-2-D6-IR	CEDAFYRYFVNLLGQGC	16.5	15.2	5.6	2.7	0.4
NNRPα-3-F6-IR	NYSQFYRYFEMLLLEGDV	19.4	18.5	6.8	2.7	0.4
NNRPα-3-H2-IR	VGDA FYRYFQGLLRQDQ	22.8	19.5	7.9	2.5	0.4
NNRPα-1-B6-IR	MHGSFYRYFQDLLQAPP	19.9	18.9	8.5	2.2	0.4
NNRPα-2-C6-IR	DVGDFYRYFGLLLTSDR	14.1	11.5	3.9	3.0	0.3
NNRPγ-4-A1-IR	NSAAFYGYFSQLLAQIR	18.4	19.2	4.1	4.7	0.2
NNRPγ-4-A7-IR	IIGGFYSYFNSVLRGT	9.7	10.9	1.8	6.0	0.2
NNRPγ-4-A9-IR	RPDPFYSYFVNLLGASA	2.5	6.3	1.3	4.9	0.2
NNRPγ-4-B11-IR	EGSGFYGYFFSLLGLQG	3.0	10.0	1.4	7.1	0.1
	LKDGFDYDFWQRLHLGS	4.1	18.7	1.2	15.5	0.1

FIGURE 2P (Con't)

Table 3C

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXLXXLXXYFXXXXX	--	--	--	--	--
rB6-4-E7-IR	LDPLDALLQYFWSVPGH	26.4	1.0	15.5	0.1	15.5
rB6-4-A12-IR	LDALDRLMRYFEERPSL	34.9	1.0	12.0	0.1	12.0
rB6-3-E6-IR	ADELEWLLDYFMHQPRP	9.0	1.0	4.8	0.2	4.8
rB6-4-E11-IR	DQELGWLRGYFEWTARD	31.2	1.6	5.9	0.3	3.7
rB6-4-F12-IR	DGVLEELFSYFSATVGP	30.4	1.0	3.4	0.3	3.4
rB6-4-D11-IR	PMNLSELWDYFRLKPGR	41.9	15.7	30.2	0.5	1.9
rB6-4-A8-IR	DSILRELRDYFAPYSHC	25.6	2.4	4.6	0.5	1.9
rB6-4-E8-IR	DDALEWLLNYFQNGHVQ	33.0	9.7	15.9	0.6	1.6
rB6-4-B9-IR	GDILDALLRYFEFGVDT	42.7	17.2	21.7	0.8	1.3
rB6-3-A6-IR	GDQLAWLLAYFQSDGSD	32.3	2.9	2.8	1.0	1.0
rB6-4-C7-IR	DGVLEGLLSYFTSTNSH	31.4	2.6	2.3	1.1	0.9
rB6-4-H12-IR	ARPLDWLLDYFKQGARG	26.0	10.0	7.2	1.4	0.7
rB6-3-C6-IR	DDMLRQLWLIFYEASAGG	34.2	19.1	12.8	1.5	0.7
rB6-4-G12-IR	DPWLAWLGRYFGETATG	37.7	6.1	3.1	2.0	0.5
rB6-4-G12-IR	DPTLFGLLRYFQESGIA	33.3	7.6	3.5	2.2	0.5
rB6-4-C11-IR	MDPLRGLLMYFSQGLV	26.6	18.7	4.7	4.0	0.3
rB6-4-G8-IR	DGLLWQLWDYFALSEHR	37.3	7.4	1.3	5.7	0.2
rB6-4-B8-IR	DNWLSALMAYFMGSGES	31.1	28.6	1.0	28.6	<0.1
rB6-4-D7-IR	DDVLNYLLGYFRQSDGL	24.1	29.4	1.0	29.4	<0.1

Figure 3C

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
RB6-4-B10-IGFR	XXXLXXLXXYFXXXXX	33.1	26.9	1.0	26.9	<0.1
RB6-3-E6-IGFR	RPVLGWLFDFVASDPM	37.6	26.6	1.0	26.6	<0.1
RB6-4-B9-IGFR	RWPLSALMDYFRRSDGV	39.2	26.3	1.0	26.3	<0.1
RB6-3-F5-IGFR	DGVLASLWRYFVSGGTL	33.2	15.6	1.0	15.6	0.1
RB6-3-B6-IGFR	DRQLGWLDYFHLTDLP	37.4	13.3	1.0	13.3	0.1
RB6-3-D4-IGFR	DGILGLLMAYFVES?RV	31.2	20.7	2.0	10.4	0.1
RB6-4-D10-IGFR	QDLLGRLWLWYFAETDTV	31.7	10.1	1.0	10.1	0.1
RB6-4-D6-IGFR	SGVLADLFRYFQRHPWP	33.9	9.9	1.0	9.9	0.1
RB6-4-F9-IGFR	DPPLGGLWTYFSRSDPG	34.3	28.3	3.0	9.4	0.1
RB6-3-E1-IGFR	DSVLRSLYSYFASGDIA	30.5	9.3	1.0	9.3	0.1
RB6-3-B2-IGFR	DGVLAALEAYFRHGPRD	22.2	8.8	1.0	8.8	0.1
RB6-3-D7-IGFR	DEILGALYSYFSLSCGA	31.2	7.6	1.0	7.6	0.1
RB6-4-C11-IGFR	QDVLGALQRYFASGEPW	33.7	7.6	1.0	7.6	0.1
RB6-4-F12-IGFR	DSVLQYLLNHFGADSKQ	38.1	7.3	1.0	7.3	0.1
RB6-4-F7-IGFR	NEVLEGLFSYFVY?ANG	38.6	7.3	1.0	7.3	0.1
RB6-3-G6-IGFR	SGILGQLLRYFKGAGGG	34.0	7.1	1.0	7.1	0.1
RB6-4-E8-IGFR	DELLDRLWQYFQVGGDL	37.6	6.9	1.0	6.9	0.1
RB6-4-G10-IGFR	PGILLDLWRYFASAPDQ	34.9	14.5	2.2	6.6	0.2
RB6-4-B12-IGFR	DSVLLDLLEYFSSGSSG	36.3	28.9	4.5	6.4	0.2
RB6-3-B5-IGFR	DGMLSRRLWEYFAGTNVP	17.2	6.1	1.0	6.1	0.2
RB6-3-C5-IGFR	DVILGGLWDYFASGGGH	38.7	15.8	2.9	5.4	0.2
RB6-4-B8-IGFR	GGVLAALERYFRVSAGD	31.9	22.0	4.1	5.4	0.2
RB6-3-H2-IGFR	DEVLGRLWAYFAQESLG	31.8	22.4	4.2	5.3	0.2
RB6-3-E5-IGFR	DGILQSLWDYFARSPVG	37.0	20.5	4.0	5.1	0.2
RB6-3-B3-IGFR	VDILSELWDYFRGEEG	31.7	4.8	1.0	4.8	0.2
RB6-4-G7-IGFR	DKVLRLLGEYFATHSKG	37.4	10.0	2.1	4.8	0.2
RB6-3-A3-IGFR	QGPLAWLRDYFASGTRS	27.2	4.7	1.0	4.7	0.2
RB6-4-E9-IGFR	QDVLRSLLSYFMNGNDV	37.3	20.1	4.8	4.2	0.2
	DGVL SKLWEYFKIQND					

Figure 3D

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXLXXLXXYFXXXXX	--	--	--	--	--
rB6-3-F1-IGFR	NTILGDLWRYFAGSGGM	26.5	5.8	1.4	4.1	0.2
rB6-4-B7-IGFR	?DVLKKL?VYFELSGGA	31.1	11.4	2.9	3.9	0.3
rB6-4-C10-IGFR	GGPLQGLYTYFKQSPVC	32.2	3.7	1.0	3.7	0.3
rB6-3-A1-IGFR	DRLLSGLWAYFAGNGGS	21.1	3.5	1.0	3.5	0.3
rB6-3-F6-IGFR	DLILQSLLDYFQGRPVG	25.1	3.5	1.0	3.5	0.3
rB6-3-H5-IGFR	LALLPMLWDYFVATDPQ	35.5	18.1	5.6	3.2	0.3
rB6-4-D8-IGFR	DSILRELRYFARTHIA	36.2	22.5	7.5	3.0	0.3
rB6-4-A8-IGFR	DGVLGQLWQYFAQYPGS	41.1	30.6	10.6	2.9	0.3
rB6-4-H8-IGFR	?PPLDALWEYFTGTARD	38.7	33.0	11.5	2.9	0.3
rB6-3-E2-IGFR	DNVLEGLWSYFALWSQL	20.9	2.2	1.0	2.2	0.5
rB6-3-C2-IGFR	SAVLEYLLAYFARTGAA	31.0	2.1	1.0	2.1	0.5
rB6-4-G8-IGFR	DRALGPLWRYFMVNNQ	38.7	5.5	2.6	2.1	0.5
rB6-3-G5-IGFR	WRILDRLLAYFKESQGD	32.8	2.0	1.0	2.0	0.5
rB6-4-C9-IGFR	DDVLVTLFQYFRASGTG	37.6	30.2	15.1	2.0	0.5
rB6-4-D11-IGFR	FDVLTWLGRYF*MNTGK	36.6	5.5	3.0	1.8	0.5
rB6-4-B11-IGFR	RDVLDGLREYFRASVGG	25.2	4.2	2.4	1.8	0.6
rB6-4-E11-IGFR	IKTLNDLLAYFRGDLDV	38.1	29.8	22.2	1.3	0.7
rB6-3-G3-IGFR	DEALLWLMRYFRGSPSP	31.6	8.7	7.2	1.2	0.8
rB6-4-H12-IGFR	ESPLDALRAYFSGRRNW	40.1	2.8	2.5	1.1	0.9
rB6-4-G12-IGFR	IQSL*DLLQYFVSSPSV	36.7	32.5	31.4	1.0	1.0
rB6-3-C4-IGFR	GGILD?LQDYFRSTDVG	37.1	6.2	13.5	0.5	2.2

Figure 3D (Con't)

Sequence alignment

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
R20β-4 - F8 - IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
	HLCVLEELFWGASLFGYCSG	39.1	1.8	27.7	0.1	15.4

Figure 4A

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
F815-4-H9-IR	HLCVLEELFWGASLFGYCSG	--	--	--	--	--
F815-3-B1-IR	PLCVLEELFWSTPLFGQCSY	34.9	0.9	37.6	<0.1	40.8
F815-3-D1-IR	HLCVLEELFWGASLFAQCVG	31.7	0.9	35.8	<0.1	39.3
F815-3-D4-IR	DLCVLEELFWGASRFGQCSG	30.4	0.9	33.5	<0.1	38.9
F815-3-C5-IR	HLCVLEELFWGASLFGQCSG	31.5	0.9	33.6	<0.1	38.8
F815-4-H3-IR	HLCVLEELFWGASLFGQCSG	31.1	0.8	31.2	<0.1	38.5
F815-3-A5-IR	NLCDLELVFWGASLFRQCSG	33.7	1.0	37.2	<0.1	38.4
F815-3-D7-IR	PLCVLEELFWGASLFGQCSG	37.4	1.1	40.9	<0.1	38.3
F815-3-A1-IR	QLCVLEELFWGASEFQCSG	33.6	0.9	34.3	<0.1	38.3
F815-4-H4-IR	HLCVLEELFWGASLFGQCSG	29.8	0.9	34.8	<0.1	38.0
F815-3-A3-IR	PLCVLEELFWGESLFGQCSG	31.1	0.9	32.7	<0.1	38.0
F815-3-B3-IR	HLCVLEELFWGASRFGQCSG	32.8	1.0	39.1	<0.1	37.9
F815-3-A4-IR	KLCVLEELFWGASLFGQCSG	33.7	1.0	37.5	<0.1	37.5
F815-3-D2-IR	YLCVLEELFWGASLFGQCSG	32.5	1.0	36.9	<0.1	37.5
F815-3-C4-IR	HLCVLEELFWGASLFAQCSG	31.9	0.9	34.1	<0.1	37.4
F815-3-B4-IR	QLCVLEELFWGESLFGQCSG	31.6	0.8	31.8	<0.1	37.4
F815-3-C1-IR	HLCVLEELFWGNLFSQCSG	33.8	1.0	36.7	<0.1	37.3
F815-4-G9-IR	HLCVLEELFWGASLYGQCSG	29.0	0.9	35.0	<0.1	37.3
F815-4-G6-IR	SLCALEEQFWGAALFGYCSG	36.5	1.0	38.9	<0.1	37.1
F815-3-A8-IR	HLCVLEELFWGASLFDGCSG	34.9	1.0	36.4	<0.1	37.0
F815-4-G5-IR	QLCVLEELFWGASLFGQCSG	34.7	1.1	39.3	<0.1	36.9
F815-3-B5-IR	PLCVLEELFWGAALFGQCSG	26.5	1.0	35.1	<0.1	36.8
F815-4-F4-IR	HLCVLEELFWGASLFGQCTG	33.2	0.9	34.1	<0.1	36.8
F815-3-A2-IR	PLCVLEELFWGASLFGQCSG	28.6	0.8	30.0	<0.1	36.7
F815-3-B6-IR	QLCVLEELFWGASLFGQCSG	32.5	1.0	36.6	<0.1	36.6
F815-4-H7-IR	HLCVLEELFWGASLFGQCSR	31.6	0.9	32.9	<0.1	36.5
F815-4-H8-IR	DLCVLEELFWGASLFGQCSG	33.7	1.0	37.6	<0.1	36.4
F815-4-G7-IR	QLCVLEELFWGASLFGQCSG	35.8	1.0	37.0	<0.1	36.4
	NLCVLEELFWGAALFGQCSG	33.7	1.0	35.8	<0.1	36.3

Figure 4B

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGF/IR	IR/IGF
F815-3-A6-IR	HLCVLEELFWGSLFGYCSG	--	--	--	--	--
F815-3-A6-IR	QLCVLEELFWGSSLFQCSG	34.6	1.1	39.0	<0.1	36.2
F815-3-D3-IR	DLCVVEELFWGKSLFGQCSG	33.8	1.0	36.2	<0.1	36.2
F815-3-B12-IR	DLCVLEELFWGSSLFQCSG	33.2	1.0	35.7	<0.1	36.2
F815-4-G10-IR	YLCVLEEQFWGASLFRQCFG	35.4	1.0	37.2	<0.1	36.1
F815-4-E3-IR	HLCVLEELLWGSSLFQCSG	32.4	1.0	35.0	<0.1	36.1
F815-4-E6-IR	PLCGLEELFWGASLFGQCSG	33.2	1.0	34.5	<0.1	36.1
F815-4-F1-IR	HLCVLEELFWGSSLFAQCSG	29.4	0.9	32.5	<0.1	36.0
F815-4-G8-IR	PLCAIEELFWGAALFGQCSG	36.8	1.1	38.2	<0.1	35.9
F815-4-H12-IR	HLCVLEEQFWGASLFGDCSG	30.5	0.9	31.9	<0.1	35.9
F815-4-G3-IR	PLCVLEELFWGAPLFGQCSG	31.4	1.0	35.7	<0.1	35.7
F815-3-C2-IR	DLCGLEELFWGAALFGQCTS	32.3	1.0	36.1	<0.1	35.6
F815-4-E10-IR	QLCVLEKQLWGASLFWQCSG	35.4	1.0	36.5	<0.1	35.4
F815-3-A12-IR	HLCVLEELFWGASLYGQCPG	32.1	1.0	36.3	<0.1	35.3
F815-3-B8-IR	HLCVLEELFWGASLFDQCSG	33.6	1.0	35.8	<0.1	35.3
F815-3-B2-IR	HLCVLEELLWGASLFGQCSG	31.0	1.0	35.3	<0.1	35.3
F815-3-C3-IR	PLCVLEELFWGVSLFGQCGG	30.1	1.0	35.3	<0.1	35.3
F815-3-A7-IR	HLCVLEELFWGASQWQCSG	33.1	1.0	35.8	<0.1	35.2
F815-4-F9-IR	RLCVLEEQFWGGALFGQCSG	33.4	1.0	35.7	<0.1	35.2
F815-3-B7-IR	QLCVLEELFWGVSLFAQCSG	32.0	1.0	33.5	<0.1	35.0
F815-4-E4-IR	HLCVLEELFWGAALFGQCFG	28.0	1.0	33.4	<0.1	35.0
F815-4-E12-IR	YLCVLEELFWGASQFGQCSG	28.0	0.9	30.2	<0.1	34.8
F815-4-F8-IR	HLCVLEELYWGASLFGQCSG	33.8	1.0	35.2	<0.1	34.7
F815-3-C7-IR	HLCVLEERFWGVSLFGQCSG	33.9	1.0	34.7	<0.1	34.7
F815-4-F10-IR	PLCVLEELFWGASRFGQCSG	32.7	1.0	34.2	<0.1	34.7
F815-3-D11-IR	HLCVLEDLFWGASLFDQCSG	35.4	1.1	37.3	<0.1	34.6
F815-4-E7-IR	HLCDLELVFWGASLFGQCSG	30.3	0.9	32.2	<0.1	34.6
F815-3-A10-IR	QLCILEEQFWGTSLFGYCSG	34.0	1.1	36.4	<0.1	34.3
F815-3-B11-IR	ALCVLEELFWGESLFGQCSG	33.7	1.1	36.3	<0.1	34.2

Figure 4B (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
	HLCVLEELFWGASLFGYCSG	--	--	--	--
F815-4-F11-IR	RLCVLEERFWGAALFGQCSG	31.8	1.0	33.7	<0.1
F815-3-A9-IR	PLCVLEELFWGASLFGQCSG	31.9	1.0	35.5	<0.1
F815-4-G11-IR	SLCVLEELFWGSRFGQCSG	32.3	1.0	34.4	<0.1
F815-3-D8-IR	HLCVLEELFWGASLFGYCFE	32.3	1.0	33.3	<0.1
F815-4-G4-IR	HLCVLEELFWGASLFGQCSG	23.8	1.0	32.2	<0.1
F815-3-C8-IR	DLCLLEELFWGSRFGQCSG	33.9	1.0	35.1	<0.1
F815-4-G12-IR	YLCVLEERFWGASLFGQCSG	31.7	1.0	33.5	<0.1
F815-3-D12-IR	HLCVLEELFWGASLFGQCSG	33.3	1.0	34.8	<0.1
F815-4-F7-IR	QLCVLEELFWGASLFGQCSG	33.3	1.0	34.3	<0.1
F815-4-F2-IR	HLCVLEELFWGASLFGYCSG	26.1	1.0	33.8	<0.1
F815-3-B9-IR	HLCVLEELFWGASLFGQCSG	33.6	1.1	35.7	<0.1
F815-4-H2-IR	PLCVLEELFWGASLFGQCSG	36.1	1.2	38.4	<0.1
F815-4-E11-IR	HLCVLEELFWGASLFGQCSG	33.2	1.1	35.4	<0.1
F815-3-A11-IR	QLCVLEELFWGASLFGQCSG	27.9	1.0	31.5	<0.1
F815-4-F6-IR	HLCVLEELFWGASLFGQCSG	37.7	1.2	40.1	<0.1
F815-3-D9-IR	HLCVLEELFWGASLFGQCSG	32.3	1.1	34.6	<0.1
F815-3-C11-IR	RLCVLEELFWGASLFGQCSG	31.4	1.0	32.5	<0.1
F815-4-G2-IR	RLCILEELFWGASLFGQCSG	33.4	1.1	35.7	<0.1
F815-3-C9-IR	HLCVLEELFWGATLFDQCSG	30.2	1.1	34.3	<0.1
F815-4-H10-IR	HLCVLEELFWGASLFGQCSG	29.7	1.0	31.4	<0.1
F815-4-F3-IR	HLCVLEELFWAAPLFGQCSG	31.9	0.9	27.6	<0.1
F815-4-F5-IR	HLCVLEELFWGASLFGQCSA	19.4	1.0	28.0	<0.1
F815-4-H1-IR	NLCVLEELFWGASLFGQCSG	12.3	0.9	24.8	<0.1
F815-4-E5-IR	PLCVLEELFWGASLFGQCSG	6.9	1.0	15.8	0.1
F815-4-H5-IR	NLCVLEELFWGASLFGQCSG	3.5	1.0	13.6	0.1
F815-3-C10-IR	QLCVLG#RFGGSLCGYCSG	5.5	1.0	13.1	0.1
	QLCVLG#RFGGSLCGYCSG	3.5	1.1	5.2	0.2

Figure 4B (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	IR/IGFR
		HLCVLEELFWGASLFGYCSC	39.1	1.8	27.7	0.1	15.4	
F815-4-F11-IGFR		PLCFLQELFGGASLGGYCSC	33.4	12.3	1.0	12.3	0.1	
F815-4-E12-IGFR		FMCGLQELVGGAAALLGHCSG	33.7	15.1	1.7	8.9	0.1	
F815-4-H10-IGFR		PLCFLQELFGGSLSGYCSC	30.1	8.5	1.0	8.5	0.1	
F815-4-B7-IGFR		FLCGLEELAWGVSRSYCFG	35.2	23.9	4.8	5.0	0.2	
F815-3-B5-IGFR		PLCFLAELFSGSALGGDCSR	33.9	4.8	1.0	4.8	0.2	
F815-4-D12-IGFR		PLCVLQELFGGSLGGYCSC	33.6	7.0	1.8	3.9	0.3	
F815-4-C11-IGFR		QLCVLE#LFWGACLFYGCAG	13.9	4.6	1.8	2.6	0.4	
F815-4-C7-IGFR		FLCGLQELSGVASLFGQCSC	16.8	2.0	1.0	2.0	0.5	
F815-4-E7-IGFR		RVCVLEQLVWGASLFGA*SG	26.9	3.8	1.9	2.0	0.5	
F815-4-G7-IGFR		FYCGLEELSWGAAALFGYCSC	30.4	9.0	5.0	1.8	0.6	
F815-4-A10-IGFR		FLCGLEELSQGAVLFGHCY	30.8	3.7	2.2	1.7	0.6	
F815-3-B3-IGFR		HLCVLVGLFWDASLFGQCSC	7.6	1.0	2.0	0.5	2.0	
F815-3-G1-IGFR		QRCIRAAALFWCATLLGGCAG	20.5	1.0	2.0	0.5	2.0	
F815-4-G12-IGFR		HQCIPDGMSQGAALRGNCSD	7.6	1.0	2.5	0.4	2.5	
F815-3-H1-IGFR		HLCVLEDELWGVSLFGYCSC	18.4	1.0	6.8	0.1	6.8	

Figure 4C

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYCSCG</u>	39.1	1.8	27.7	0.1	15.4
F820-4-B5-IR		HLCMLEEQFWGASLFSRCSG	28.1	0.9	17.9	<0.1	21.1
F820-4-A2-IR		TCAFWKNGSGVRRCSVTAVV	34.0	1.6	22.7	0.1	13.9
F820-4-E2-IR		PLCGLKN.SGVRLCSSPALV	21.3	0.7	9.0	0.1	13.4
F820-4-D10-IR		PLCLQEELFWGASLFGYCSCG	34.1	1.0	12.1	0.1	12.1
F820-4-H7-IR		PLCDLEELFWGASLFGDCPG	14.2	0.6	6.5	0.1	11.6
F820-4-G6-IR		DLCVLEELFWDGSLFASCSG	14.0	0.5	6.1	0.1	11.5
F820-4-C2-IR		PLCVLEELQWGTALFGSCTG	38.1	1.2	11.8	0.1	9.9
F820-4-B4-IR		PLCLVEELLMGASLFSQCTG	15.1	0.7	6.4	0.1	8.7
F820-4-C7-IR		PLCDLEELYWGAALFGSCSG	46.3	2.7	22.2	0.1	8.2
F820-4-F10-IR		GLCFLEEQFWGTSLFRDCPG	14.5	0.6	4.7	0.1	8.0
F820-4-G5-IR		PLCVVEELFWGASLYGQCSG	8.8	0.6	4.4	0.1	7.5
F820-4-F2-IR		RLCVLEELFWGASRFRGCSG	11.7	0.6	4.2	0.1	7.4
F820-4-H8-IR		PLCVLEELHWGAALFGYCSCG	16.0	0.6	4.7	0.1	7.3
F820-4-D7-IR		NLCVVEELFWGASLFPNCSG	14.5	0.8	5.9	0.1	7.1
F820-4-B2-IR		QLCVLEELFWGASMFEDCSG	5.0	0.4	2.4	0.2	6.9
F820-4-C3-IR		HLCVLEEQFWGASLFGQCSG	37.5	1.1	7.5	0.2	6.6
F820-4-H4-IR		PLCVLEELIYWGAALFGDCYG	21.2	1.1	6.4	0.2	5.9
F820-4-B10-IR		PLCVLEELFWGLSLDKNCS	7.5	0.7	3.7	0.2	5.6
F820-4-A5-IR		QLCVLEELFWGASLFSGCSG	5.3	0.8	4.4	0.2	5.2
F820-4-F6-IR		PLCDLEALFWGESLFGGCSG	5.7	0.6	3.0	0.2	4.9
F820-4-F1-IR		HLCVLEEMFWGTSHFDGCSG	9.1	1.0	4.7	0.2	4.7
F820-4-A3-IR		DLCVLEELFWGAPLFGLCSCG	5.9	0.8	3.5	0.2	4.5
F820-4-D1-IR		DLCVLEELFWGVALYGGCSG	25.7	2.3	10.5	0.2	4.5
F820-4-F5-IR		QLCVLEELYWGAALFGHCSG	3.7	0.6	2.7	0.2	4.2
F820-4-F12-IR		HLCVLEDRFWGASLFGPCSG	11.3	0.6	2.2	0.3	3.5
F820-4-A11-IR		HLCGMEEMFWGVALFRNCSG	7.6	0.8	2.7	0.3	3.5
F820-4-E8-IR		PLCVLEQLYWGESLFFVYCSG	8.0	1.2	4.3	0.3	3.5
F820-4-H3-IR		HLCVLEELFWGEALWGYCSG	17.5	2.6	9.0	0.3	3.4

Figure 4D

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYCSG</u>	--	--	--	--	--
F820-4-A8-IR		QLCVMEELFWGASRFGQCSG	6.4	0.7	2.4	0.3	3.4
F820-4-G1-IR		HLCVLEELFWGASMFQCSG	3.9	0.6	1.9	0.3	3.4
F820-4-F3-IR		QLCVLEEMFWGGSFVQCSA	9.8	1.3	3.6	0.4	2.9
F820-4-D6-IR		PLCILEELFWGEALFDQCGA	5.4	1.2	3.2	0.4	2.6
F820-4-A1-IR		YLCVQEELFWGASLFGYCSV	25.5	2.4	6.1	0.4	2.5
F820-4-H2-IR		HLCALAEAFPGPSLFNSCQG	15.9	1.6	4.1	0.4	2.5
F820-4-F4-IR		HLCVLEERFWGASLFGQCSG	6.8	1.9	4.7	0.4	2.5
F820-4-B6-IR		QLCDLEELFWGASLFGYCPG	4.1	0.8	1.9	0.4	2.4
F820-4-B11-IR		HLCVLEERFWGASLFGYCSG	22.2	3.1	7.0	0.4	2.3
F820-4-H6-IR		QLCVLEELFWGASLFGYCSG	4.1	1.1	2.4	0.5	2.2
F820-4-H9-IR		PLCVLEELFWGAAQFGQCSR	3.1	0.9	1.9	0.5	2.1
F820-4-D3-IR		QLCDLEERFWGASLFGYCSG	4.6	1.3	2.5	0.5	1.9
F820-4-C1-IR		QLCVLEEVFWGASLFGYCSG	13.0	1.1	2.1	0.5	1.9
F820-4-D12-IR		QL.DLNTWSGLCLCSVTVRV	10.4	1.2	2.0	0.6	1.7
F820-4-B8-IR		DLCVLEESLWGKALFGYCSG	7.2	2.2	3.4	0.6	1.5
F820-4-C6-IR		HLCVLEEVFWGSSMFGDCSG	13.9	2.5	2.8	0.9	1.1
F820-4-C10-IR		HLCVLEELFWGASLFGDCQG	5.3	2.6	2.9	0.9	1.1
F820-4-D4-IR		QLCVLDALMWGGRGLGHQCG	3.5	2.3	2.1	1.1	0.9
F820-4-E1-IR		QLCVLEEKFWGTSLFGDCMG	1.6	1.6	1.5	1.1	0.9
F820-4-B3-IR		HLCVLEEVFWGAAQFGSCSG	15.9	0.6	5.0	1.2	0.8
F820-4-D2-IR		QLCVLEELFWGSPMFGYCSG	7.8	3.2	2.5	1.3	0.8
F820-4-C5-IR		HLCVLEELFWGASGFAQCYG	21.5	4.0	2.3	1.8	0.6

Figure 4D (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-C4-IR	HLCVLEELFWGASLFGYCSCG	--	--	--	--	--
A6L-3-D7-IR	DLCVLEERFWGASLFGQCSCG	36.9	1.0	40.5	<0.1	42.5
A6L-3-A1-IR	QLCVLEELHWGASLFGYCSCG	38.6	1.0	40.1	<0.1	40.7
A6L-3-C1-IR	PLCVLEEQFWGASLFGQCSCG	39.6	1.1	44.8	<0.1	40.6
A6L-3-D5-IR	YLCDLEERFWGASLFGQCSCG	37.3	1.0	40.3	<0.1	40.3
A6L-3-A4-IR	HLCVLEELFWGASLFGQCSCG	42.9	1.1	44.4	<0.1	40.2
A6L-3-D3-IR	HLCVLEELFWGASLFGQCSCG	26.7	1.1	42.2	<0.1	40.2
A6L-3-B1-IR	HLCVLEERFWGASLFGQCSCG	34.6	0.9	36.9	<0.1	39.8
A6L-3-B5-IR	HLCVMEELFWGTSLFGQCTG	33.9	1.0	38.7	<0.1	39.3
A6L-3-B2-IR	HLCVLEERFWGASLFGQCSCG	35.3	1.1	42.4	<0.1	38.6
B6H-4-G12-IR	HLCVLEERFWGASLFGQCSCG	38.1	1.1	42.7	<0.1	37.7
B6C-4-H10-IR	HLCVLEELFWGASLFGQCSCG	31.6	1.1	39.6	<0.1	36.7
B6H-4-G8-IR	QLCVLEELFWGASLFGQCSCG	38.5	1.1	41.1	<0.1	36.5
A6L-3-D6-IR	HLCVLEEMFWGASLFGQCSCG	31.7	1.1	39.7	<0.1	36.2
B6C-4-F1-IR	HLCVLEELFWGASLFGQCSCG	35.5	1.0	37.2	<0.1	36.1
B6C-4-H3-IR	QLCVLEELFWGASLFGQCSCG	32.9	1.1	38.7	<0.1	35.8
B6H-4-E8-IR	QLCVLEELFWGASLFGQCSCG	37.4	1.2	40.5	<0.1	34.8
B6C-4-G1-IR	QLCVLEELFWGASLFGQCSCG	30.2	1.0	35.7	<0.1	34.3
B6H-4-E9-IR	HLCVLEEFWGDLSLFGQCSCG	34.9	1.2	40.2	<0.1	33.7
B6C-4-F5-IR	HLCVLEERFWGASLFGQCSCG	34.4	1.2	38.8	<0.1	33.2
B6C-4-F11-IR	QLCVLEELFWGASLFGQCSCG	34.7	1.2	39.6	<0.1	32.8
B6C-4-E6-IR	HLCVLEELFWGASLFGQCSCG	34.0	1.2	37.2	<0.1	31.7
B6C-4-E12-IR	HLCVLEELFWGASLFGQCSCG	32.3	1.2	37.4	<0.1	30.6
B6C-4-G10-IR	HLCVLEELFWGASLFGQCSCG	30.9	1.1	33.3	<0.1	30.2
B6C-4-F8-IR	HLCVLEELFWGASLFGQCSCG	33.0	1.3	40.3	<0.1	30.1
20C-3-B5-IR	QLCVLEEQFWGASLFGNCSCG	36.4	1.4	39.8	<0.1	29.3
B6C-4-G3-IR	HLCVLEERFWGASLFGQCSCG	26.6	1.1	32.5	<0.1	29.2
20C-3-B7-IR	HLCVLEEMFWGASLFGQCSCG	34.0	1.4	38.8	<0.1	28.3
	PLCVLEELVWGASLFGQCSCG	29.5	1.2	32.9	<0.1	28.3

Figure 4E

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-B4-IR	HLCVLEELFWGASLFGYCSCG	28.9	1.1	31.1	<0.1	28.0
20C-3-C11-IR	NLCVLEELFWGESLFGQCSG	30.2	1.1	31.0	<0.1	27.7
B6C-4-G2-IR	HLCVLEEQFWGGSFLFGYCSR	29.4	1.3	35.3	<0.1	27.5
20C-3-B8-IR	HLCFLEEVFWGAALFAQCSG	28.5	1.1	31.2	<0.1	27.4
20C-3-C10-IR	HLCDLELVFWGSALFGQCSG	32.1	1.2	33.6	<0.1	27.1
20C-3-B6-IR	HLCVMEELFWGASLFGQCSG	29.7	1.2	31.9	<0.1	26.7
A6L-3-A3-IR	HLCVLEERFWGASLFWQCSG	14.4	1.1	28.3	<0.1	26.5
A6L-3-B3-IR	HLCVLEEQYWGESLFGYCSCG	38.7	1.7	43.4	<0.1	26.3
20C-3-A5-IR	PLCVLEEQFWGASLFAYCSC	22.9	1.1	27.6	<0.1	26.0
20C-3-B11-IR	QLCVLEELFWGESLFAQCLG	30.0	1.3	32.7	<0.1	25.8
20C-3-B3-IR	HLCVLEELFWQSLFGHCSD	29.3	1.2	31.2	<0.1	25.7
20C-3-C12-IR	HLCVLEELVWGASLFGFCSCG	29.6	1.3	31.8	<0.1	24.8
20C-3-C3-IR	LLCVLEEQFWGASLFGQCSG	30.1	1.2	30.1	<0.1	24.3
20C-3-C2-IR	RLCVLEELFWGESLFGQCSG	29.9	1.3	29.8	<0.1	23.8
20C-3-A11-IR	ELCFLEELFWGASLFGQCSG	25.9	1.2	27.4	<0.1	23.0
20C-3-A4-IR	HLCVLEELFWGASLYGQCSS	27.2	1.2	27.5	<0.1	22.9
20C-3-A6-IR	HLCVLEELFWGASLFAQCPG	26.1	1.2	27.5	<0.1	22.8
B6C-4-E4-IR	NLCVLEELFWGASEFQCSG	34.5	1.7	39.1	<0.1	22.7
20C-3-A9-IR	DLCVLEEQWGSALFRYCSCG	29.7	1.3	29.3	<0.1	22.7
B6C-3-C5-IR	HLCVLEEQFWGVALFGNCSCG	33.5	1.7	37.7	<0.1	22.5
20C-3-B1-IR	HLCVLEEQWGSALFGQCSG	30.2	1.2	26.7	<0.1	22.0
20C-3-A10-IR	HLCVLEERFWGGALFGQCTA	29.0	1.3	28.5	<0.1	21.5
20C-4-F1-IR	HLCDLEELFWGASLFGQCSG	29.1	1.4	29.5	<0.1	20.7
20C-4-E1-IR	QLCVLEELFWGTSLFAGCSG	28.3	1.4	29.7	<0.1	20.6
20C-3-B12-IR	QLCVLEELFWGASLFGYCSCA	27.0	1.3	25.8	<0.1	20.2
20C-3-A8-IR	HLCVLEELFWGASLFGQCSS	21.1	1.1	21.2	0.1	20.0
20C-3-A7-IR	FLCVLEELVWGASQFQCSG	21.9	1.3	23.0	0.1	18.3
B6C-4-E10-IR	HLCVLEEQFWGASLFGYCSCG	35.2	2.2	38.0	0.1	17.5

Figure 4E (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20C-3-A1-IR	HLCVLEELFWGASLFGYCSCG	21.0	1.1	17.6	0.1
20C-3-C1-IR	RLCALEELFWGASLFGQCSG	30.6	1.4	21.9	0.1
A6L-3-D2-IR	HLCVLEELFWGAALFHQCSG	7.0	1.1	14.9	0.1
B6C-4-G12-IR	RLCVLEEQFWGASLFGQCSG	31.1	2.5	33.5	0.1
B6H-4-F9-IR	QLCVLEELFWGSSRLGYCSG	39.3	3.6	43.1	0.1
B6C-4-E3-IR	DLCVLEELFWGASLFGQCSG	34.6	5.3	40.0	0.1
20C-3-B10-IR	QLCLLEEQFWGSLFGQCSG	29.9	16.9	31.7	0.5
20C-3-A3-IR	HLCVLEELFWGTSLFGQCSG	28.4	19.1	25.3	0.8
	RLCVLEELVWGASLFDQCSR				1.3

Figure 4E (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYC</u> SG	39.1	1.8	27.7	0.1	15.4
F815-4-D10-IGFR		PLQALCEKFFGAWMFGYC	31.2	13.9	1.0	13.9	0.1
F815-4-H11-IGFR		HLQVLCELFGGVYLFGYC	27.2	19.2	1.7	11.3	0.1
F815-4-C8-IGFR		PLFDLCELFGGASLSGYC	35.4	17.4	1.6	10.9	0.1
F815-4-E8-IGFR		HL*ALCELFGGVNSFGYCVG	29.5	16.9	1.7	9.9	0.1
F815-4-E11-IGFR		QLGVLCMFGGAFRLGYCQ	36.6	25.7	2.7	9.5	0.1
F815-4-A7-IGFR		HLQDLCELFGGAYLFGYC	29.6	16.0	3.8	4.2	0.2
F815-3-D3-IGFR		QLQVLCELFGGAVSLRLLLW	33.7	3.5	1.0	3.5	0.3
F815-4-F7-IGFR		PLGVLCCEQFGGAFRFGYC	33.6	18.9	9.9	1.9	0.5
F815-4-A9-IGFR		PL*GLCELFGGASLFGYC	7.5	1.7	2.3	0.7	1.4
F815-4-B12-IGFR		DLRVLCELFGGAYVLGYCSE	35.1	3.7	12.6	0.3	3.4

Figure 5

Clone Parental/Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D815-4-A8-IR	WLDQEWAWVQCEVYGRGCP	44.8	1.4	24.2	<0.1	17.3
D815-4-A8-IR	WLDLEWAQVQCEVYGRGCP	48.0	1.0	48.4	<0.1	48.4
D815-4-D10-IR	WLDQEWAWVQCEVYGRGCP	49.2	1.0	48.2	<0.1	48.2
D815-4-D9-IR	WLDQEWQVQVQVYGRGCT	47.5	1.0	48.0	<0.1	48.0
D815-4-A11-IR	RLDEEWARVQCEVYGRGCR	47.9	1.0	48.0	<0.1	48.0
D815-4-E12-IR	WLEQEWAWIQCEVYGRGCP	49.0	1.0	47.6	<0.1	47.6
D815-4-B7-IR	WLEQEWAWVQCEVYGRGCP	45.4	1.0	47.2	<0.1	47.2
D815-4-D11-IR	WLDDEEWIQCCKVYGRGCP	49.5	1.0	47.0	<0.1	47.0
D815-4-D12-IR	WLEQEWAWVQCEVYGRGCS	48.1	1.0	46.6	<0.1	46.6
D815-4-F8-IR	WLDQEWAWIQCEVYGRGCP	47.8	1.0	46.4	<0.1	46.4
D815-4-A9-IR	SLDQEWAWIQCEVYGRGCP	47.7	1.0	45.8	<0.1	45.8
D815-4-E9-IR	WLEQEWQVRLVYGRGCP	47.8	1.0	45.8	<0.1	45.8
D815-4-B10-IR	WLDQEWAWVQCEVYGRGCP	49.0	1.0	45.6	<0.1	45.6
D815-4-H8-IR	WLDQEWAGVLCEVYGRGCP	47.0	1.0	45.6	<0.1	45.6
D815-4-E10-IR	SLDKEWVLCVYGRGCP	44.5	1.0	45.6	<0.1	45.6
D815-4-D7-IR	WLEQEWAWVQCEVYGRGCR	44.2	1.0	45.4	<0.1	45.4
D815-4-G9-IR	WLEEWAWVQVAVYGRGCS	44.2	1.0	44.2	<0.1	44.2
D815-4-G12-IR	WLDQEWALVQCEVYGRGCP	44.3	1.0	43.7	<0.1	43.7
D815-4-E11-IR	WLDQEWAWVQCEVYGRGCP	45.5	1.0	43.0	<0.1	43.0
D815-4-H7-IR	WLEQEWAWVQCEVYGRGAS	46.2	1.0	43.0	<0.1	43.0
D815-4-F12-IR	WLDQEWAWVECEVYGRGCP	47.2	1.0	42.6	<0.1	42.6
D815-4-E8-IR	WLDQEWAWVEQVYGRGCP	47.9	1.0	42.6	<0.1	42.6
D815-4-F9-IR	QLDQEWAWVLCVYGRGCP	46.4	1.0	41.8	<0.1	41.8
D815-4-A10-IR	WLDHE*AWVQCEVYGRGCP	47.3	1.0	41.2	<0.1	41.2
D815-4-C7-IR	QLEQEWAWVRCEVYGRGCS	37.7	1.0	40.0	<0.1	40.0
D815-4-H10-IR	WLDQEWAWVQVQVYGRGCL	47.0	1.0	39.8	<0.1	39.8
D815-4-C9-IR	WLDQEWAWVRCEVYGLGCP	44.2	1.0	39.8	<0.1	39.8
D815-4-F11-IR	WLDQEWAWMKCELYGRGCP	40.4	1.0	39.2	<0.1	39.2
D815-4-H12-IR	WLEQEWAWVQCEVYGRGCL	45.4	1.0	38.6	<0.1	38.6
D815-4-A7-IR	SLDQEWAWVQCEVYGRGCL	37.3	1.0	37.3	<0.1	37.3
D815-4-H11-IR	WLDHEWAWVQCEVYGRGCT	2.4	1.0	37.2	<0.1	37.2
D815-4-F7-IR	WLDVEWAWVQCEVYGRGCP	32.4	1.0	34.7	<0.1	34.7

Figure 6B

Clone	Parental/Design	Sequence	Ratios over Background		Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
D815-4-G8-IR		WLDQEWAWVQCEVYGRGCP	--	--	--	--
D815-4-G7-IR		QLDQEWARVRCEVWGRGCSS	27.8	1.0	33.6	<0.1 33.6
D815-4-G11-IR		WLDLEWAQVQCKVYGRGCP	34.7	1.0	32.3	<0.1 32.3
D815-4-E7-IR		WLDEEAWVQCVYGRGCP	30.7	1.0	28.6	<0.1 28.6
D815-4-A12-IR		WLDQEWAWVQCEVWGRGCAF	33.0	1.0	26.4	<0.1 26.4
D815-4-B11-IR		WLDREWAQVQCEVYGRGCLS	28.4	1.0	19.0	0.1 19.0
D815-4-D8-IR		WLDAEWEVQCEVYGRGCRP	22.1	1.0	18.8	0.1 18.8
		SLDREWAYVQCQVYGRGCSS	20.8	1.0	14.6	0.1 14.6

Figure 6B (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D820-3-D5-IGFR		WLDQEWAWVQCEVYGRGCPS	44.8	1.4	24.2	0.1	17.3
D820-3-E4-IGFR		WVNQALGGVQSDVQRRQCS	29.6	3.8	1.0	3.8	0.3
D820-3-C5-IGFR		LLDHEWPWVGCEVCGRGSLS	27.1	3.2	1.0	3.2	0.3
D820-3-F4-IGFR		WLHQELAWVRGEGYPRGRRS	25.0	3.1	1.0	3.1	0.3
D820-3-F6-IGFR		WLGHDWAWIQCEVYGLGCPC	3.9	2.7	1.0	2.7	0.4
D820-3-G4-IGFR		WIDQEGVRVQCEA*GRAFPS	26.7	2.6	1.0	2.6	0.4
D820-3-E2-IGFR		WRDEEWAWVQGVQGRGWA	3.8	2.6	1.0	2.6	0.4
D820-3-G6-IGFR		RLGVESWFRKVYGRDSTS	15.3	2.6	1.0	2.6	0.4
D820-4-E11-IGFR		WLAQGWAGVQCIVYGRGCRN	20.3	2.4	1.0	2.4	0.4
D820-4-H11-IGFR		WLEEE*AGIQCV?GRGCPS	12.6	1.0	3.0	0.3	3.0
D820-4-D11-IGFR		WLDQEWVQVRCVYGRGCPS	8.1	1.0	4.6	0.2	4.6
D820-4-A8-IGFR		WLEEEWAQVQCIVYGRGCAS	4.5	1.0	5.3	0.2	5.3
D820-4-F9-IGFR		WLDLE*EWLQCEVYGRGCAT	3.2	1.0	5.5	0.2	5.5
D820-4-C8-IGFR		WLEEEWAQVQCIVYGRGCPS	9.4	1.0	5.8	0.2	5.8
D820-4-D7-IGFR		WLDQEWVQVRCVYGRGCPS	11.6	1.0	5.9	0.2	5.9
D820-4-H9-IGFR		WLEEEWAQVQCIVYGRGCPS	10.1	1.0	8.9	0.1	8.9
D820-4-E10-IGFR		WLDQEWVQVRCVYGRGCPS	34.1	3.5	33.4	0.1	9.5
D820-4-E7-IGFR		YLD?EWAWVQCEVYGLGCQS	18.4	1.0	10.1	0.1	10.1
D820-4-A11-IGFR		WLDVE*AWVQCEVWGRGCPS	26.7	2.6	27.0	0.1	10.4
D820-4-B10-IGFR		WLEQEWER?QCEVYGRGCPP	31.9	3.0	32.2	0.1	10.7
D820-4-F10-IGFR		WLEEEWAQVQCIVYGRGCPS	16.1	1.0	11.7	0.1	11.7
D820-4-B9-IGFR		WLDQEWAWIQCEVYGRGCPS	8.0	1.0	12.5	0.1	12.5
D820-4-G8-IGFR		?LEHEWAQIQCEV?GRGCQS	19.6	1.0	14.9	0.1	14.9
D820-4-E9-IGFR		WL?QEWAWIQCEVYGRGCPF	19.3	1.0	17.3	0.1	17.3
D820-4-B10-IGFR		WLD?EWAWVQCEVYGRGCPS	19.3	1.0	21.5	<0.1	21.5
D820-4-F10-IGFR		GLEQGCPCWVGLVQCRGCPS	27.8	1.0	25.7	<0.1	25.7
D820-4-B9-IGFR		WLEEEWAQVQCIVYGRGCPS	31.7	1.0	26.5	<0.1	26.5
D820-4-G8-IGFR		WLDQEWAWIQCEVYGRGCSS	25.6	1.0	29.3	<0.1	29.3

Figure 6D

	Sequence	HIR affinity mol/l
J228	HPPLEHLKAFLN-NH ₂	2.4*10 ⁻⁵
J229	APTFYAWFNQQT-NH ₂	2.4*10 ⁻⁶
S122	HPSTKEIYAKLLK	9.3*10 ⁻⁶
S123	HPSTNQMLMKLFK	1.6*10 ⁻⁵
S124	HPPLSELKLFLLKK	2.3*10 ⁻⁵

Figure 7

J-nr	Sequence	HIR affinity mol/l
J101	ACVWPTYWNCG	$5.0 \cdot 10^{-6}$
J103	Ac-CVWPTYWNCG	$3.0 \cdot 10^{-5}$
J104	Bz-CVWPTYWNCG	$3.2 \cdot 10^{-5}$
J105	Ac-ACVWPTYWNCG	$4.5 \cdot 10^{-5}$
J109	ACVWPTYWACG	$2.0 \cdot 10^{-5}$
J110	ACVWPTYANCG	$2.4 \cdot 10^{-5}$
J111	ACVWPTAWNCG	$3.1 \cdot 10^{-5}$
J112	ACVWPAYWNCG	$3.3 \cdot 10^{-5}$
J113	ACVWATYWNCG	$5.5 \cdot 10^{-5}$
J115	ACAWPTYWNCG	$2.7 \cdot 10^{-6}$
J116	AAVWPTYWNAG	$3.4 \cdot 10^{-5}$
J117	ASVWPTYWNSG	$2.9 \cdot 10^{-5}$
J118	ACPYNWWTWCG	$2.9 \cdot 10^{-5}$
J119	ACVWPTYWnCG	$3.2 \cdot 10^{-5}$
J120	ACVWPTYwNCG	$3.4 \cdot 10^{-5}$
J121	ACVWPTYWNCG	$1.8 \cdot 10^{-5}$
J122	ACVWPIYWNCG	$5.1 \cdot 10^{-5}$
J123	ACVWpTYWNCG	$2.5 \cdot 10^{-5}$
J124	ACVwPTYWNCG	$2.0 \cdot 10^{-5}$
J125	ACvWPTYWNCG	$1.8 \cdot 10^{-5}$
J127	acvwptywncg	$4.4 \cdot 10^{-5}$
J128	gcnwytpwvca	$5.3 \cdot 10^{-5}$
J130	AEVWPTYWN(Dpr)G	$1.9 \cdot 10^{-5}$
J131	ACoWPTYWNCG	$5.5 \cdot 10^{-5}$
J132	AC(Leu)WPTYWNCG	$4.5 \cdot 10^{-6}$
J133	AC(dLeu)WPTYWNCG	$2.8 \cdot 10^{-5}$
J134	AC(Ile)WPTYWNCG	$7.4 \cdot 10^{-6}$
J135	AC(dIle)WPTYWNCG	$2.9 \cdot 10^{-5}$
J136	AC(Met)WPTYWNCG	$7.5 \cdot 10^{-6}$

FIGURE 8

J137	AC(dMet)WPTYWNCG	$2.5 \cdot 10^{-5}$
J138	AC(ABu)WPTYWNCG	$7.8 \cdot 10^{-5}$
J139	AC(dABu)WPTYWNCG	$2.1 \cdot 10^{-5}$
J140	AC(Nva)WPTYWNCG	$3.6 \cdot 10^{-6}$
J141	AC(dNva)WPTYWNCG	$3.0 \cdot 10^{-5}$
J142	AC(tBuG)WPTYWNCG	$3.2 \cdot 10^{-5}$
J143	AC(dtBuG)WPTYWNCG	$3.8 \cdot 10^{-5}$
J144	AC(Phe)WPTYWNCG	$5.1 \cdot 10^{-6}$
J145	AC(dPhe)WPTYWNCG	$5.7 \cdot 10^{-5}$
J146	AC(Cha)WPTYWNCG	$2.2 \cdot 10^{-5}$
J147	AC(dCha)WPTYWNCG	$1.7 \cdot 10^{-5}$
J148	AC(Nal(1))WPTYWNCG	$5.8 \cdot 10^{-6}$
J149	AC(dNal(1))WPTYWNCG	$2.0 \cdot 10^{-5}$
J150	AC(Acy)WPTYWNCG	$2.0 \cdot 10^{-5}$
J151	ACVWPT(Hyp)WNCG	$2.2 \cdot 10^{-4}$
J154	ACVWPT(Nal2)WNCG	$8.2 \cdot 10^{-5}$
J155	ACVWPT(MetO ₂)WNCG	$1.9 \cdot 10^{-4}$
J157	ACVWPT(Cha)WNCG	$1.2 \cdot 10^{-4}$
J160	ACVWPT(Ser)WNCG	$1.8 \cdot 10^{-4}$
J162	ACVWPT(Thi)WNCG	$2.5 \cdot 10^{-4}$
J163	ACVWPT(dSer)WNCG	$5.0 \cdot 10^{-5}$
J166	ACVWPT(dCha)WNCG	$7.5 \cdot 10^{-5}$
J170	ACVWPT(dPhe)WNCG	$1.4 \cdot 10^{-4}$
J171	ACVWPT(Thr)WNCG	$7.7 \cdot 10^{-4}$
J174	ACVWPT(Phe)WNCG	$4.5 \cdot 10^{-5}$
J176	ACVWPT(dThr)WNCG	$2.8 \cdot 10^{-5}$
J180	ACVWPTYW D CG	$5.6 \cdot 10^{-5}$
J182	ACVWPT D WNCG	$2.7 \cdot 10^{-5}$
J183	ACVWP D YWNCG	$3.3 \cdot 10^{-5}$
J184	ACVW D TYWNCG	$6.2 \cdot 10^{-5}$

Figure 8 (Con't)

J185	ACV _D PTYWNCG	$3.4 \cdot 10^{-5}$
J186	AC _D WPTYWNCG	$3.5 \cdot 10^{-5}$
J187	ACVWTYWNPCG	$4.3 \cdot 10^{-5}$
J188	ACVWTYWPNCG	$3.0 \cdot 10^{-5}$
J189	ACVWTPYWNCG	$3.1 \cdot 10^{-5}$
J190	ACVWTPYWNCG	$2.6 \cdot 10^{-5}$
J191	ACVPWTYWNCG	$3.0 \cdot 10^{-5}$
J192	ACPVWTYWNCG	$4.2 \cdot 10^{-5}$
J193	ACWPTYWNVCG	$4.8 \cdot 10^{-5}$
J194	ACPTYWNVWCG	$4.2 \cdot 10^{-5}$
J195	ACTYWNVWPCG	$3.3 \cdot 10^{-5}$
J196	ACYWNVWPTCG	$2.4 \cdot 10^{-5}$
J197	ACWNVWPTYCG	$2.9 \cdot 10^{-5}$
J198	ACNVWPTYWCG	$4.2 \cdot 10^{-5}$
J199	ACVWPCG	$4.7 \cdot 10^{-5}$
J200	CVWPTYWNCG	$5.5 \cdot 10^{-5}$
J201	ACWWPTYWNCG	$6.8 \cdot 10^{-6}$
J202	ACEWPTYWNCG	$4.6 \cdot 10^{-6}$
J203	ACRWPTYWNCG	$5.8 \cdot 10^{-6}$
J204	ACQWPTYWNCG	$9.2 \cdot 10^{-6}$
J205	ACGWPTYWNCG	$4.4 \cdot 10^{-6}$
J207	cyclo-Valeroyl-AWPTYWNCG	$5.5 \cdot 10^{-5}$
J208	cyclo-ToluyI- AWPTYWNCG	$7.6 \cdot 10^{-5}$
J209	cyclo-Acetyl- AWPTYWNCG	$7.7 \cdot 10^{-5}$
J210	(WPTYWNCG) ₂	$5.3 \cdot 10^{-5}$
J211	(AWPTYWNCG) ₂	$7.9 \cdot 10^{-6}$
J212	ACA(Bpa)PTYWNCgK(biotin	$1.8 \cdot 10^{-5}$
J213	ACAWPTY(Bpa)NCGK(biotin	$1.8 \cdot 10^{-5}$
J214	GCAWPTYWNCG	$1.4 \cdot 10^{-6}$
J215	NCAWPTYWNCG	$9.0 \cdot 10^{-6}$

Figure 8 (Con't)

J216	VCAWPTYWNCG	$2.8 \cdot 10^{-6}$
J227	SFYEAHQLLGV-NH ₂	$6.4 \cdot 10^{-6}$
J228	HPPLEHLKAFLL-NH ₂	$2.4 \cdot 10^{-5}$
J229	APTFYAWFNQQT-NH ₂	$2.4 \cdot 10^{-6}$
S122	HPTSKEIYAKLLK	$9.3 \cdot 10^{-6}$
S123	HPSTNQMLMKLFK	$1.6 \cdot 10^{-5}$
S124	HPPLSELKLFLIKK	$2.3 \cdot 10^{-5}$

Figure 8 (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
H5 Parental	LCQSLGVITYPGWLAGWCA	--	1.2	--	--
H5-3-JBA5-IGFR	LCQSWGVRIGWLAGLCP	31.9	16.3	--	--
H5-3-E1A11-IGFR	VCQSLGITDLGLCAGWGA	21.3	8.0	--	--
H5-3-E4B10-IGFR	LCQSLGLTHPGFEAWLCA	29.7	7.8	--	--
H5-3-E4C10-IGFR	LCQNFQVTDPGCFYGFWA	24.3	6.1	--	--
H5-3-JBB6-IGFR	PCQRLGDTLHCWLAGWFA	40.2	5.4	--	--
H5-3-E4A9-IGFR	LCQSSGLSFLGCLGWWA	27.7	4.3	--	--
H5-3-E2A12-IGFR	LCQSLGFTDLDLACWFE	27.2	4.2	--	--
H5-3-E4A12-IGFR	VCQGLGVECPGWFAWGA	27.9	3.9	--	--
H5-3-E1F9-IGFR	PCQSLGLTCSGWFEWGA	18.6	3.5	--	--
H5-3-E4F11-IGFR	LCQGWGIRIGWLVGRM	28.4	3.3	--	--
H5-3-E4A11-IGFR	LWQSVGIKYPGGLAGWLA	31.0	3.0	--	--
H5-3-E4G7-IGFR	QWQSLGVTCPGSWAELCA	26.2	2.2	--	--
H5-3-E1B9-IGFR	LCQSLGVITYWEGLAWLCA	20.0	2.1	--	--

Figure 9A

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
JBA5 Parental	LCQSWGVRIGWLAGLCP	31.5	20.6	1.0	20.6	<0.1
JBA5-4-2C12-IGFR	LCQSWGVRIGWLAGLCP	46.8	41.5	1.0	41.5	<0.1
JBA5-2-1F9-IGFR	LCESWGVRIGWLAGLCP	48.1	39.5	1.0	39.5	<0.1
JBA5-2-1E10-IGFR	LCQSWGVRIGWLVGLCP	42.5	39.5	1.1	35.9	<0.1
JBA5-4-2A11-IGFR	LCQSWGVRIGWLAGLCP	44.1	40.2	1.2	33.5	<0.1
JBA5-3-2A3-IGFR	LCQSWGVRIGWLVGLCP	34.7	33.3	1.0	33.3	<0.1
JBA5-4-2A9-IGFR	LCQSWGVRIGWLTGLCP	34.6	33.1	1.0	33.1	<0.1
JBA5-1-1B6-IGFR	MCQSWDVRIGRLGGQCP	39.6	31.4	1.0	31.4	<0.1
JBA5-4-2B9-IGFR	LCQGWDRIGQLAGLCP	39.6	22.3	1.0	22.3	<0.1
JBA5-1-1H7-IGFR	LCQGWDRIGWLAGLCP	24.9	22.6	1.2	18.8	0.1
JBA5-3-2C3-IGFR	LCQSWDVRIGWVAGLCP	35.5	15.3	1.1	13.9	0.1
JBA5-1-1G7-IGFR	LCQSWDARIGWLAGLCP	26.2	14.8	1.5	9.9	0.1
JBA5-2-1E9-IGFR	LCLG*DVRIGLLAGLCP	39.4	4.5	1.0	4.5	0.2
JBA5-2-1D12-IGFR	L*KSVDVRSGLMAGLCP	42.2	2.2	1.0	2.2	0.5

Figure 9B

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
JBA5-4-G12-IR	LCQSWGVRIGWLAGLCP	--	--	--	--	--
JBA5-4-G3-IR	LCQSWDACIQWLVLGLSP	37.5	3.0	1.4	2.1	0.5
JBA5-4-G1-IR	LCRSWEECIGWLVPQP	4.5	2.5	1.1	2.3	0.4
JBA5-3-B1-IR	LCQSWGECIDRLVGQGA	32.0	3.2	1.3	2.5	0.4
JBA5-3-C1-IR	LCQGWGVRIGWLAGLCP	29.4	6.8	1.2	5.7	0.2
JBA5-3-A6-IR	LCQGWAVHIGQLAGLCP	36.3	7.5	1.1	6.8	0.1
JBA5-3-A2-IR	LCQGWGVHIGRLAGLCP	28.0	7.4	0.7	10.6	0.1
JBA5-3-B7-IR	LCQSWGVRIGWLAGLCP	10.2	4.8	0.4	12.0	0.1
	LCQSWGVRIGRLAGLCP	39.2	15.2	1.2	12.7	0.1

Figure 9C

Sequence

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R20-4-C10-IGFR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
	PKGTRFRGDDVDVWDGYSWLA	37.8	3.8	--	--

Figure 10A

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20F-4-H10-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
20F-4-C10-IR	LDLASGDSWLGYDVLRGWLS	10.2	3.1	2.4	1.3	0.8
	IHSSDGIGAWGGYAWFRDVA	23.4	9.6	4.1	2.3	0.4

Figure 10B (Con't)

Figure 10C

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20β-4-D10-IR	LGPLLRWGSEVCGVWPDLC	21.5	1.0	8.0	0.1	8.0
R20β-4-D9b-IR	PFGGGRWWGIPRMWWYRNS	32.6	6.8	15.1	0.5	2.2
R20β-4-H4-IR	WWGGRNRWWLERWGLGGER	11.6	1.7	3.6	0.5	2.1
R20β-4-A2-IR	GRVALWGPVWPRWWFMSRPV	17.1	2.6	5.2	0.5	2.0

Figure 10C

Figure 10D

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
R40-3-40A2-IR R40-4-40F10-IR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
	RGTRDRLWKSGGFAIVPRWPCFSYHCLVEWITKTGSPG	44.6	1.5	2.7	0.6	1.8
	GRTSMAFVPPRHLQPELAPRPVRNHAWLVG	46.4	1.9	2.1	0.9	1.1

Figure 10D

Sequence Alignment

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R20-4-F10-IGFR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
R20-4-F7-IGFR	CLGAGSFRAGILCLGLPVS	35.5	6.0	--	--
R20-4-H9-IGFR	GFWATACGGLQICEELGLKP	29.1	4.7	--	--
R20-3-A4-IGFR	DLFCAYMAQAALGLGQDLSCG	25.7	3.0	--	--
	RHLLLPQIWIAS*GGWGMG	15.6	2.7	--	--

Figure 10E

Clone	Sequence	Ratios over Background			Comparisons	
Design		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-H3-IGFR	xxxxcxxxxxxxxxxxxxxxxxxxxx	--	--	--	--	--
20C-3-F4-IGFR	DHRLCGTDEYLMQDLFVRGLCLTIW	28.5	26.6	1.0	26.6	<0.1
20C-4-C10-IGFR	GLLFCQKQFTLAGLQPEAGCVSSSR	34.4	27.5	1.2	23.1	<0.1
20C-3-G5-IGFR	IWIACLDLRLRGQVWSSCRRRAPIG	35.5	24.4	1.3	19.2	0.1
20C-3-A2-IGFR	DWLRCLGVILSGGLTELANTGCVQG	29.3	21.1	1.1	18.7	0.1
20C-3-B4-IGFR	WFSFCLGGLLQAQEWVWGRDVGCI	33.9	18.3	1.1	16.9	0.1
20C-3-C6-IGFR	GYSWLRDVLMEKQALKREGSVGRQ	39.8	29.1	1.9	15.2	0.1
20C-3-E2-IGFR	FLTRLERLGLS*ERGEAGGPIYAQA	34.8	20.9	1.4	14.9	0.1
20C-3-A3-IGFR	FSGFCMGLERLSQVSLGYCGAGQGG	34.8	28.1	2.0	14.2	0.1
20C-3-B1-IGFR	ISFRCQLFVLAGMHPCPVDVGGEGF	33.7	14.3	1.2	12.4	0.1
20C-3-F5-IGFR	NTPNCSQDWQESGFMAILLALTCK	30.2	9.8	0.9	11.2	0.1
20C-4-A7-IGFR	LQGFCELLATVTGTGLGCLDYQPI	35.5	31.9	3.9	8.2	0.1
20C-4-F8-IGFR	GSSICNLLARAQIVELALCEMGVQE	33.3	19.3	2.8	6.9	0.1
20C-4-G11-IGFR	LSFACLLSQLSGVVLPDCLLGED	30.5	27.7	5.3	5.2	0.2
20C-3-E1-IGFR	GEHFCQLLMSLCGDDCGPVNCGGGS	24.7	13.3	2.8	4.7	0.2
20C-3-B6-IGFR	GWFECLLASLVLPQGRSRASAVC	34.0	5.1	1.6	3.1	0.3
	YRQECACSVGAVGFLCGLCLARSG	37.3	32.8	13.7	2.4	0.4

Figure 10F

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
NNKH-2-C5-IGFR		HLSVLEELSWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1
NNKH-2-D9-IGFR		HL*VLEELSWGASLVGQWAV	7.3	0.9	0.7	1.3	0.8
NNKH-2-H12-IGFR		HLSVLEEL*LGASMFGLWAG	4.1	0.5	0.4	1.3	0.8
NNKH-2-D10-IGFR		HLSVLKELSW*ASLFGQWAG	5.0	1.3	1.1	1.2	0.8
NNKH-2-G9-IGFR		HLSALEELSWGASLFGQWAG	4.8	2.1	1.9	1.1	0.9
NNKH-2-C6-IGFR		HLSVLAELS*GALLFGQWAG	1.9	1.4	1.3	1.1	0.9
NNKH-2-C7-IGFR		RLSVLEQLSWGASLFGPWAG	18.2	1.0	0.9	1.1	0.9
NNKH-2-F11-IGFR		HL*VLVQPSWGASLFGQWAG	21.8	1.3	1.3	1.0	1.0
NNKH-2-H3-IGFR		HQSVLEELSR*ASLFGQWAG	6.7	1.3	1.4	0.9	1.1
NNKH-2-B8-IGFR		DMSVLGGLSWGA*LFGQWSG	4.7	0.7	0.8	0.9	1.1
NNKH-2-B12-IGFR		HLSVREGQLWRASMFGRWAG	17.5	3.7	5.2	0.7	1.4
NNKH-2-F9-IGFR		QLSVLVEL*WGASLFGPWAA	1.2	1.0	2.9	0.3	2.9
		HLSVGEELSW*VALLGQWAR	3.7	0.6	2.1	0.3	3.5

Figure 10I

D Name	Clonal Name	Formula #	K _d (μM) HIR	PO ₄	Fat Cell Assay	Activity	K _d (μM) HIGFR	Ratio IGF/IR	Sequence
D101	20D3	1	0.51 0.27				13 11	25 41	KIGGGQHQDGNFYDFWFEALAKK (ε-biotin)
D102	20D1	1	1.2 0.97				7.4 16	6.2 16	KVLQARHGCDSSVSDCFYEWFAKK (ε-biotin)
D103	B8	1	0.74				15	20	KWSALLSVMDTGFYAWFDDAVKK (ε-biotin)
D104	E7	1	20				>20	>1	KGISWALVRHVDRLLFYEFDLKK (ε-biotin)
D105	H8	1	2.8				12	4.3	KRDKPTDQEEQNSFYEFWRHKK (ε-biotin)
D106	20F1	1	0.97				6.2	6.4	KVFWNCRSQQLDFYEWFEQAACK (ε-biotin)
D107	40G11	1	1.1	YES		Antagonist	9.7	8.8	KLESHYVVPQAAALDRLLFYSWFSKK (ε-biotin)
D108	3G11	1	2.3			Antagonist	19	8.3	KFYGWFSRQSLTPRDDWGLPKK (ε-biotin)
D109	20H1	1	3.6			Antagonist	12	3.3	KSAPGLVSNKQDGLFYSWFREKK (ε-biotin)
D110	G3	1	0.84			Antagonist	1.4	1.7	KRGGGTIFYEFWFSALRKHGAGKK (ε-biotin)
D111	D2	1	0.62				3.2	5.2	KDPERMQSDVGFYEFWFRAAVGGKK (ε-biotin)
D112	IGFR C1 A65-4-C1	1	0.49 0.19			Neutral	0.05* 0.02*	0.1 0.1	DYKDCWARPCGDAANFYDFWVQQASKK (ε-biotin)
D113	IGFR I12								
D114	A65-4-1+2	1	0.75		~20 μM	Agonist	5.4	7.2	DYKDVFTTSVFIENFYDFWVRQVSKK (ε-biotin)
D115	IGFR A6	1	8.1			Neutral	>20	>2.5	SAKNFYDFWVKK (ε-biotin)
D116	IGFR D5	1	8.1				>20	>2.5	ADKNFYDFWMAAKK (ε-biotin)
D117	IGFR JBA5	9	4.4 cycli		>20 μM	Agonist	8.1	1.8	DYKDLCSQSWGVRIQWLGLCPKK (ε-biotin)
D118	IGFR I12C	1	0.70	YES	~20 μM	Agonist	6.1 5.1	8.6 8.5	FIENFYDFWVRQVSKK(ε-biotin)
D119	20E2	2	0.25	YES	~20 μM	Agonist	1.3	5.2	DYKDFYDAIDQLVRGSARAGGTRDKK (ε-biotin)
D120	20C11	2	0.25	YES	~20 μM	Agonist	13 2.5	2.9 0.8	KDRAFYNGLRDLVGA VYGAWDKK (ε-biotin)
D121	E8	10	0.37			Antagonist	2.2	5.9	KVRGFGGTVWPGYEWLRNAKK (ε-biotin)
D122	F2	10	1.1			Antagonist	7.4	6.7	KSMFVAGSDRWPGYGVLAADWLKK (ε-biotin)
D123	20A4 (A7)	6	1.2 1.0			Antagonist	>20 >20	>17 >20	KEIEAEWGRVRLVYGRVCVGGKK (ε-biotin)
D124	D8	6	0.55 1.3			Antagonist	16 >20	29 >15	KWLDQEWAWVQCEVYGRGCPSSKK (ε-biotin)
D125	F8	4	0.04* 0.09*				8.2 >20	200 >200	KHLCLVLEELFWGASLFGYCSGKK (ε-biotin)
D126	IGFR E4	1	2.6				>20	>8	DYKDERSAAGFRGNFYDFWFAQVNNKK (ε-biotin)
D127	IGFR D2C	1	1.4				18	13	LGENFYDFWVQMVRKK

Figure 11A

Clonal Name	D or S name	Motif	Sequence	IR-Kd	IR-IC ₅₀ Blatcore	IR-IC ₅₀ FP-S175	PO ₄	Fat Cell Assay
20-E2	D118	B6	DYKIDFYDAIDQLVRSARAGGTRDK K-biotin	250 nM		2.8 nM	+	++
C1	D112	A6	DYKDCWARPCGDAANFYDWFVQQAS KK-biotin	490 nM			-	0
D8	D123	C-C 100P	KWL DQEWAWVQCVYGRGCPSKK	550 nM			0	-
E8	D120	GROUP 6	KRGFGGTWPGYEWLRNA	370 nM			-	-
F8	D124	C-C 100P	KHLCVLEELFWGASLFGYCSGKK	40 nM			-	0
I2C	D117	A6	FHEIFYDWFVROQVSKK	700 nM	>5 µM	5 nM	++	++
KCF9			RLYYEWFWGQLEAQGRGLS					
KC-G2		C-C-C	GLEQGCPCWVGLVQCRGCPSS					
KCG7		B6	FYCGLEELSWGAAALFGYCSG		<1 µM			
NG-C2		B6	GNIGDMFYQLLSLVGRDMH					
NG-G33		A6	GLISQSPESFYDWFAGQVSDPWWCW		2-4 µM	4.2 nM	+++	
NG-G8		B6	VEGRGLFYDILRQLLARRQNG		>5 µM		-	
NG-G9		B6	RAMSFYDALVSLGLCPKK-Biotin		1 µM		+	
RP-1		A6	GSRPVFIEQFYEWFDQLGL		1 µM		+	
RP-2		A6	RSEASFIVEFYSWFEEQLRS		>10 µM		-	
RP-3		A6	GRFYGWFDQDAIDQLMPWGF		5 µM		+	
RP-4		B6	PPWGARFYDAIEQLVFDNL		6 µM		-	
RP-5		B6	AGVNAGFYRYFSTLIDWWDQGGK-Biotin				++++	
RP-6		B6 + C-C	TFYSCLASLLTGTPQNRGPWERCRRK-Biotin					
RP-7		A6	AAVIEQFYDWFADQYKK					
RP-8		B6	QSFYDYIEELIGGEWKK		>5 µM		+	
RP-8#	S287	B6	QSFYDYIEELIGGEWEE					
RP-9		A6	GSIDIESFYDWFERQLGKK			2.9 nM	++	
RP-10		B6	GSFYELQRLVGGEQGGK		>10 µM		+	
RP-11		A6	QAPSNFYDWFVREWDKK		>10 µM		+	
RP-12		B6	DPFYQGLWEWLRESGKK					
RP-13		A6	ASGFPEFYDWFGRQLSLKK		>10 µM			
RP-14		A6	SACQFDCHEFYDWFARQKK					
RP-15		A6	SQAGSAFYAWFDQVLRITVKK					
RP-16		B6	V.DARDDJFJULSEVTL					
RP-17		B6	QSDAFYSGLWALIGLSDGKK		>10 µM			
RP-18		B6	LQPCSGFYECIERLIGVKK					
RP-19		A6	LKDGFDYDFWQRLHLGSKK					
RP-20		B6	GSASFYDAIDRLRMRIKK					
RP-24		GROUP 6	WPGYLFEEALQDWRGSTD					
S167	S167	A6	AFYDWF-AKK	>20 µM	No Binding		-	
S173	S173	RB6	LDALDRLMRYFEERPSL	1.2 µM				-
S174	S174	RB6	PLAELWAYFEISEQGRSSAH	16 µM				0
S175	S175	A6	GRVDWLQRANFYDWFVAELG	230 nM	2.4 µM	0.9 nM	++	0
S176	S176	A6	NGVERAGTGDNFYDWFVAQLH	470 nM				+++

Figure 11B

Clonal Name	D or S. name	Motif	Sequence	IR-Kd	IR-IC ₉₆ Blacore	IR-IC ₉₆ FP-S175	PO ₄	Fat Cell Assay
S177	S177	B6	EIIWNTVDFFYFTLFEWLRESG	2.7 μ M				+
S178	S178	B6	EIIWNTVDFFYQYFSELLRESG	130 nM				0
S179	S179	A6	QSDSGTVIHDRFYGWFRTDWTAS	540 nM				++
F8-C12	S224	C-C LOOP	FQSLLEELVWGAPLFRYGTG					
S225	S225	C-C LOOP	PLCVLEELFWGASLFGYCSCG					
D8-G1	S226	C-C LOOP	QLEEWAGVQCEVYGRCPSP					
S264	S264	A6	IQGWEPFYGWFDVVAQMFEF					
S257	S257	B6	RWPNFYGFESLITIFS					
S258	S258	B6	HYNAFYEFQVLLAETW					
S259	S259	B6	EGWDFYSYFSGLLASVT					

Figure 11B (Con't)

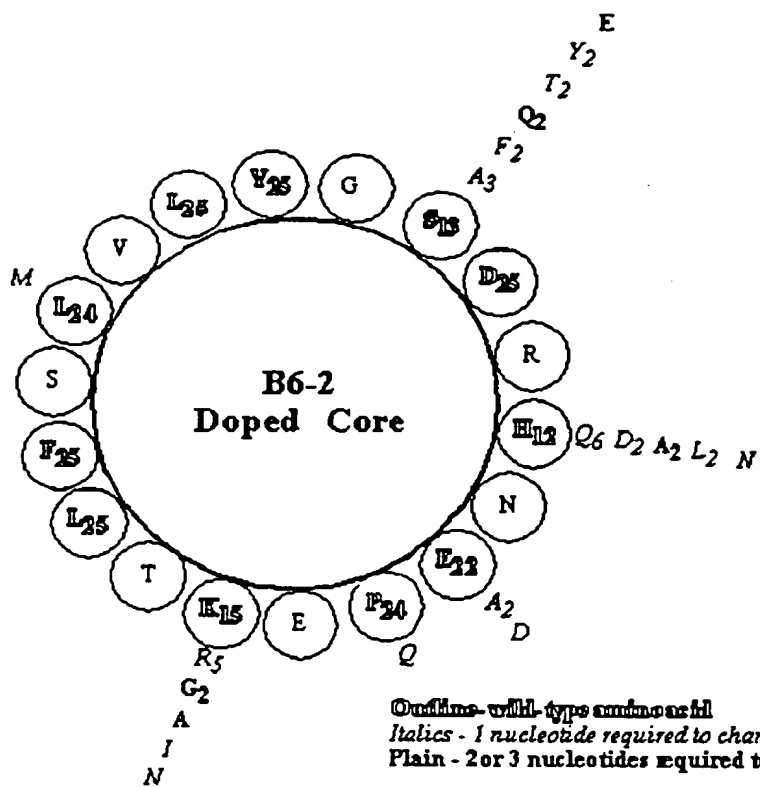


FIGURE 12

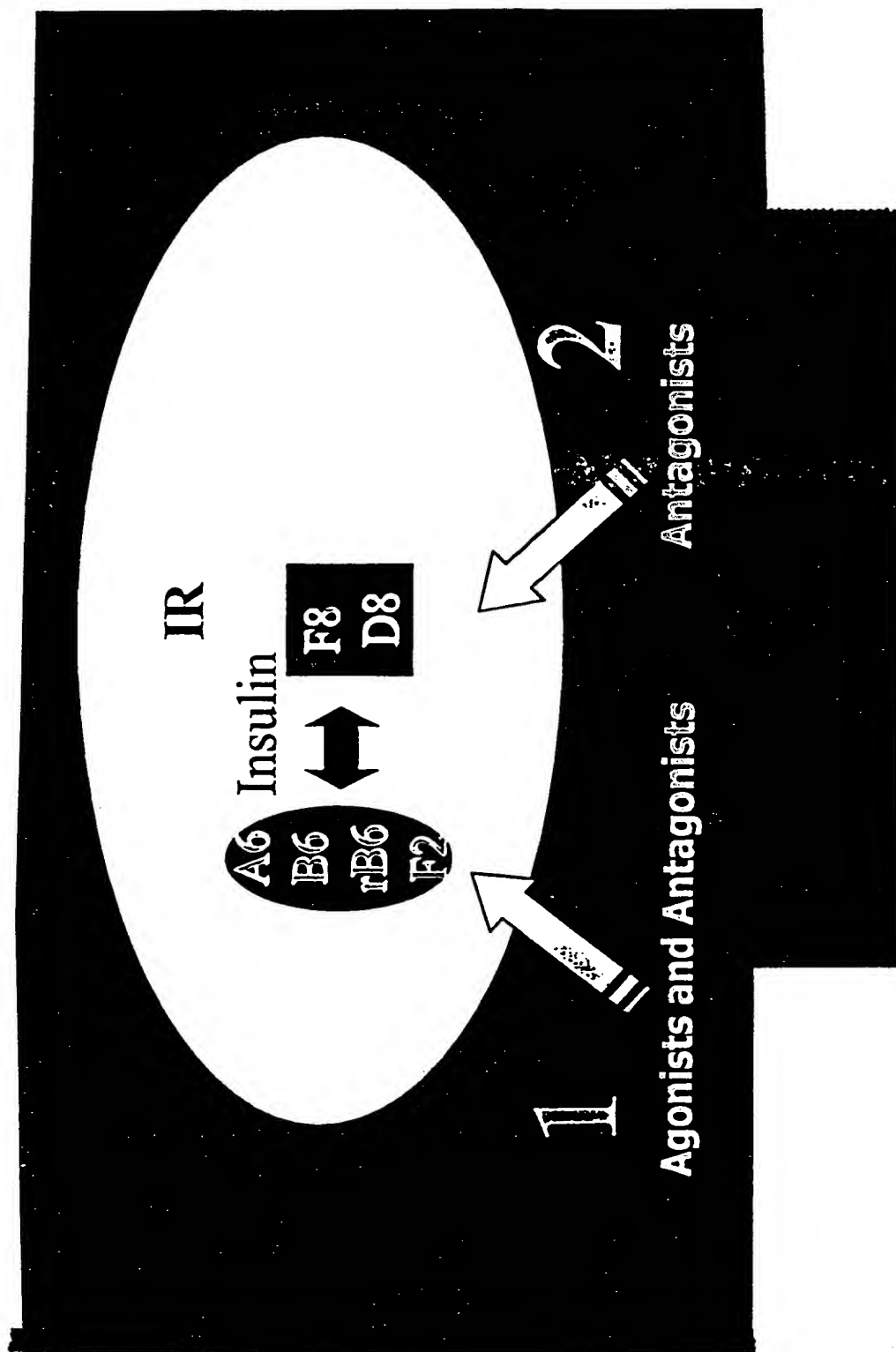


FIGURE 13

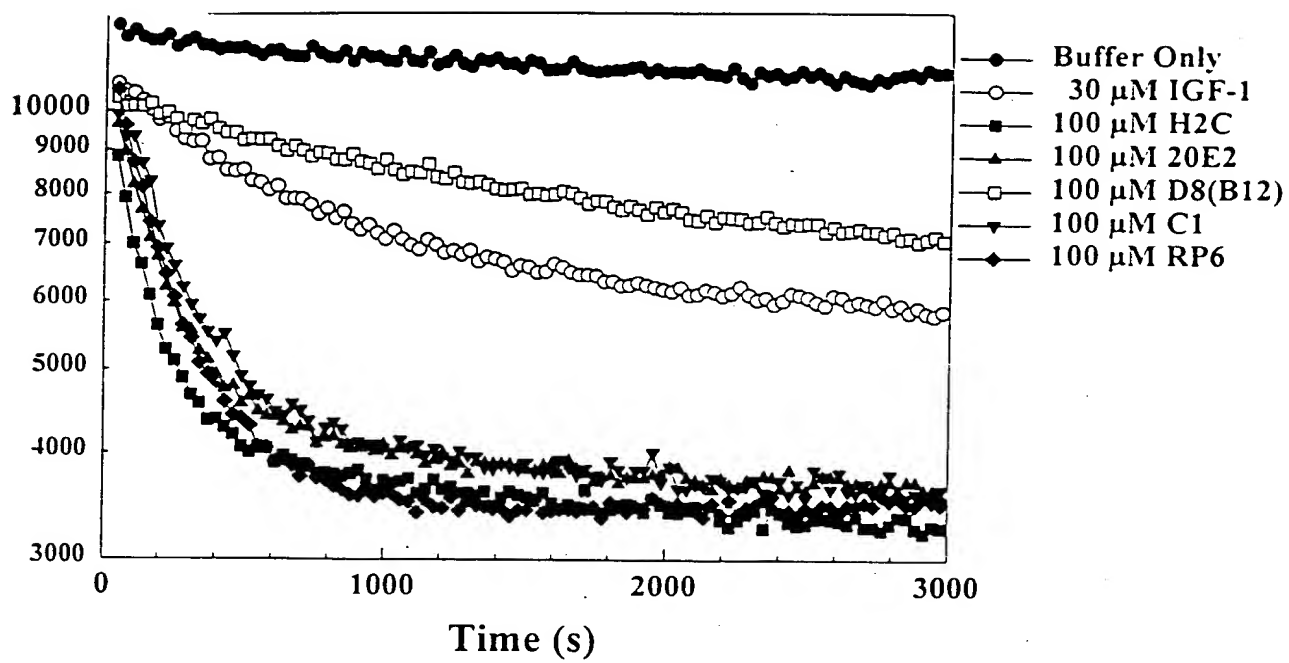


FIGURE 14

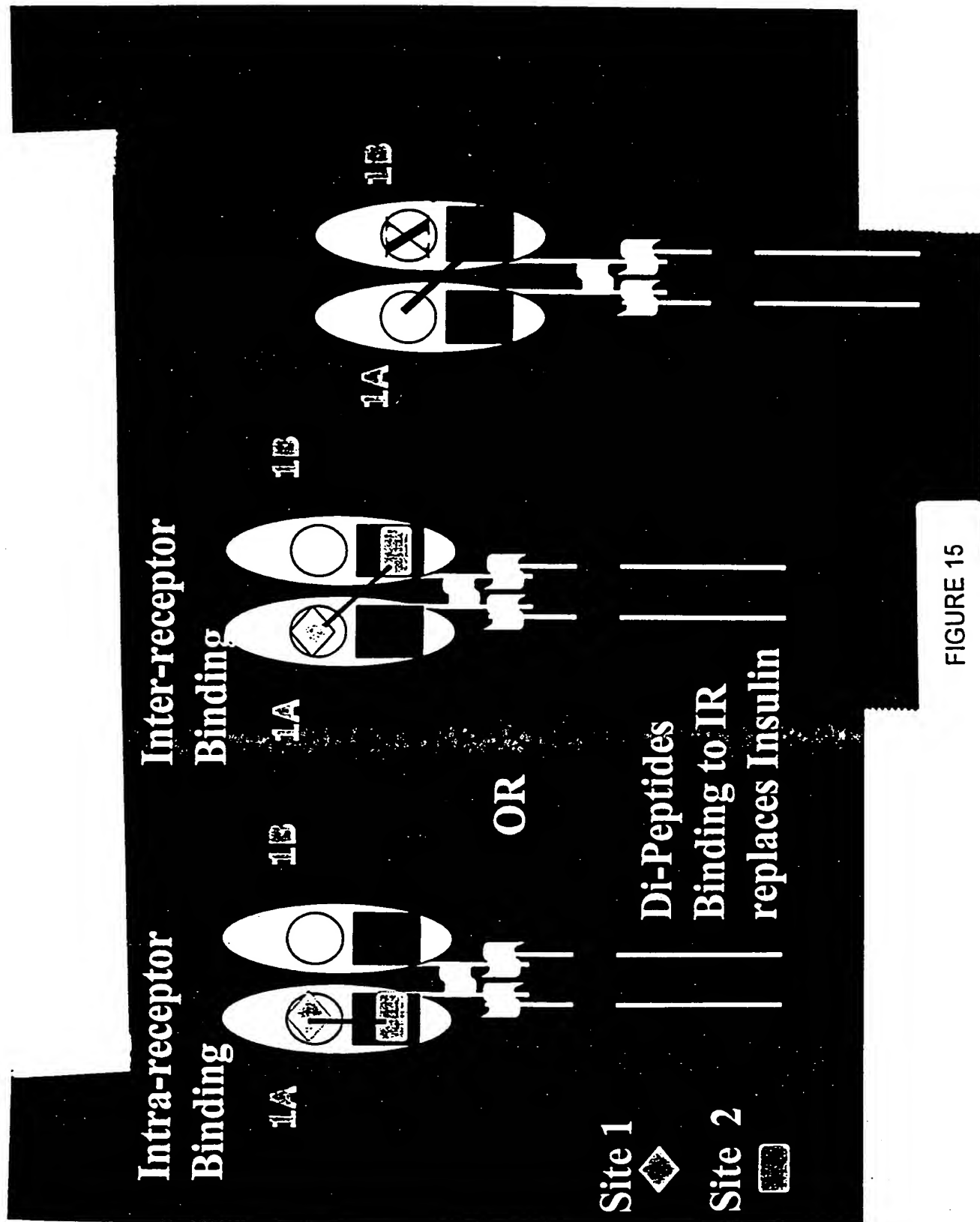


FIGURE 15

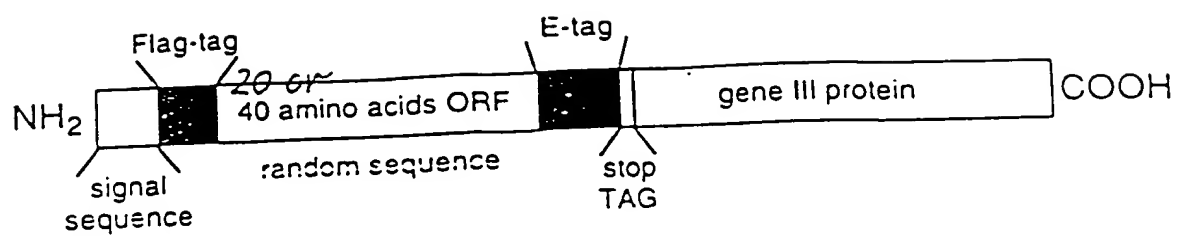


FIGURE 16

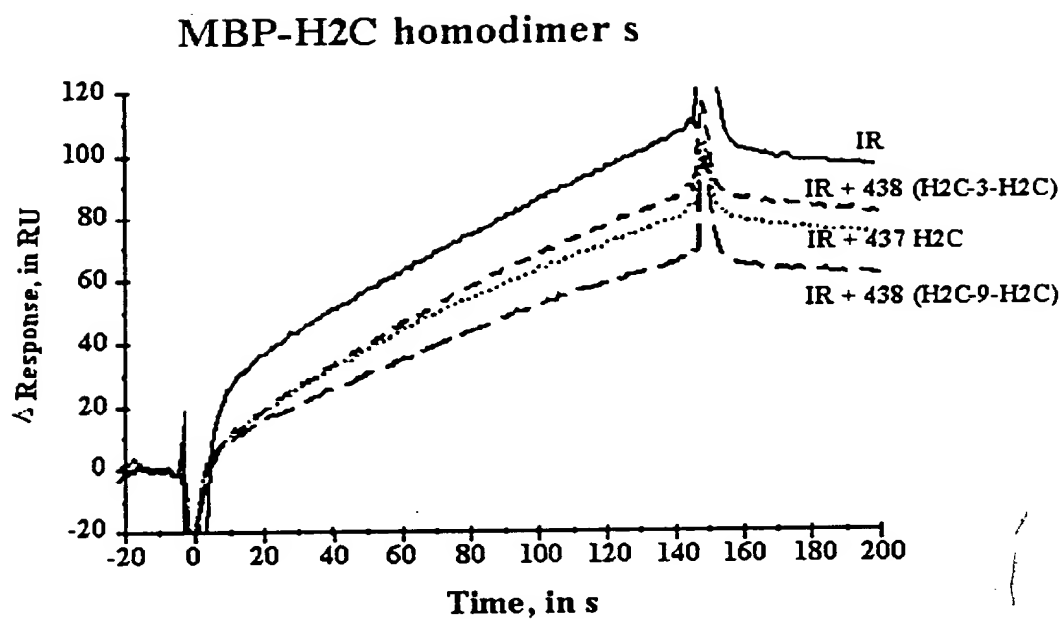


FIGURE 17

IGF-5

GACTACAAAG ACTGCTGGGT GAATTTTCGG TAIGTTCCTG GCGTGCTTA GGTTCAGAT TCTTCTGGG CCGTTCTCA AGATTGCTG TCACATGAAA GATATTTT ATTCGTGTT GCGTAGTTG GCGGCCGCA 139
D Y K D S M L N F R Y V A G R A Q V S D S S V A V S . G L C S D E R Y F L F V V G Q F G G R
T T K T R G . I F G M L L G V L R F Q I L L M P F P K D C V Q M K D I F Y S L L A S L A A A
L Q R L V V L F S V C C W A C L G F R F F C G R F L R I V F R . K I F F I R C W L V W R P

IGF-8

GACTACAAAG ACCGGTGG GCGTGTCTT GCTCTTGGG GGTGATGAC CTTTATATG GCTTCTCGT ATCGTATG GTCGTGGGTC TCGGCCGCA 100
D Y K D A V A A A V A P W G . . A F L M A S P Y A D W S W V C G R
T T K T R L R L L L L L G G D E P F Y G L L R M L I G R G S A A A
L Q R R G C G C C C S L G V M S L F M G F S V C . L V V G L R P

IGF-15

GACTACAAAG ACTGCTGGT TTGCTGGGT GTGATGATTA GCTTTTCTG TTATAGGGGT CCGTGGCTT TTTTACTAG CCGTGGCTG CTTGTGCTG TCCATATG CTTCTTGTG GTGTGCTG GCGGCCGCA 139
D Y K D W L V C L G V M I S F F C L G G R C G F L L S V G C L V V C P Q C F F G V W C G G R
T T K T G W F A W V . . L A F S V Q G V G V A F Y S A L A A L L C A H S A S I V C G A A A
L Q R L V G L L G C D D Q L F L F R G S V M L F T Q R W L P C C V P I V L L W C V V R R P

IGF-7

GACTACAAAG ACCGGATG GGTGTGTAG CTGATAGT TGGGTGGA GGGGTATG ATGGCTGAT GGGTTTATG CCGTCTGCT GCGGCCGCG CA 112
D Y K D P D W V L Q L I S L G L E G M Q I G . W V L C V F D G A G W G G R
T T K T R I G C C S . L V W G W R G C R L A D G F Y A F L M A L A G A A A
L Q R P G L G V V A D Q F G V G G D V D W L H G F H R F . W R M L G R P

FIGURE 19

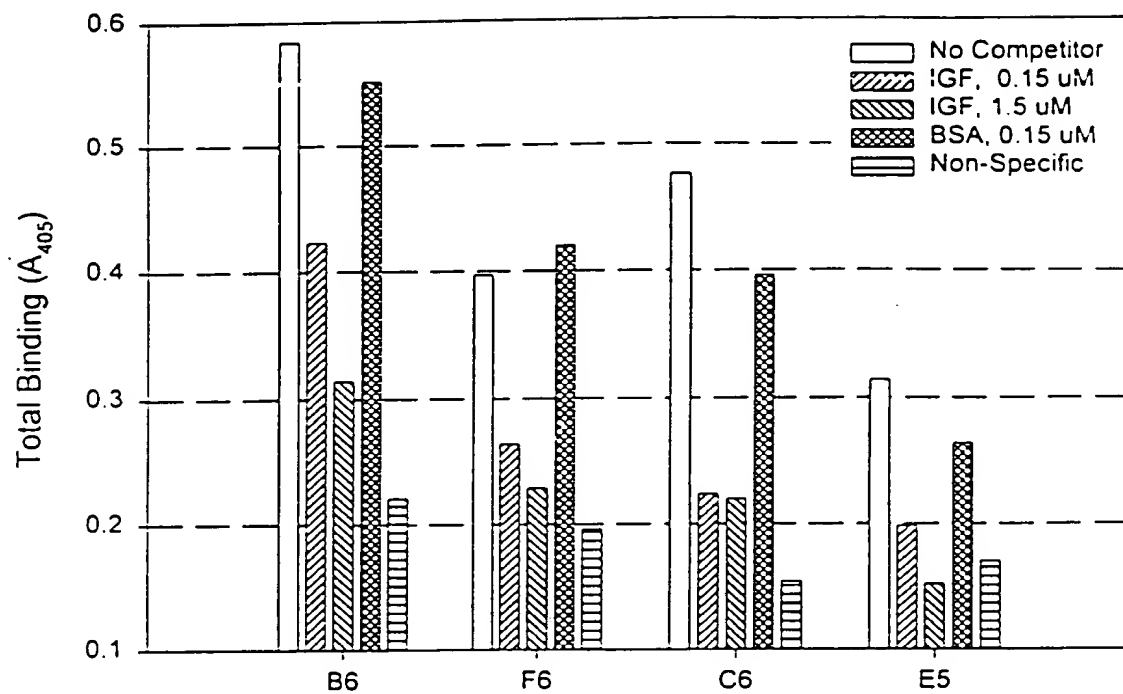


FIGURE 20A

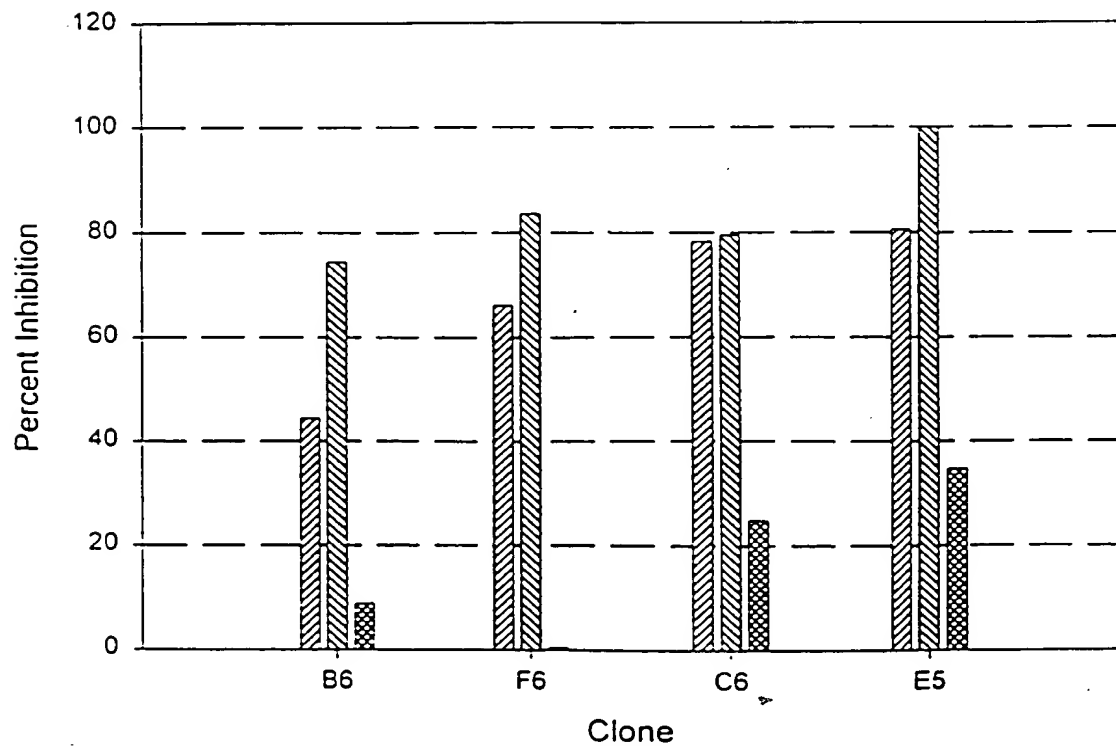


FIGURE 20B

Sequence

Clone B6	AETPAQVGNRLWSVWPGEHWNTVDPFYHKLSELLRESGA
Peptide 5.1 (18 aa)	NTVDPPFYHKLSELLREKK (biotin)
Clone F6	MLLGVLRFQILLWPPFKDCVQMKDIFYSLLASL
Peptide 5.2 (17 aa)	QMKDIFYSLLASLAAKK (biotin)
Clone D5	PLYGGGIHLIYPGTMGYVPGFPRQVKVLGDADKNFYDWFEM
Peptide 5.3 (14 aa)	ADKNFYDWFMAAKK (biotin)
Clone A6	YRGMLVLGRISDGAGKVASEPPARIGQKVFVNFYDWFV
Peptide 5.4 (12 aa)	SAKNFYDWFVKK (biotin)

FIGURE 21

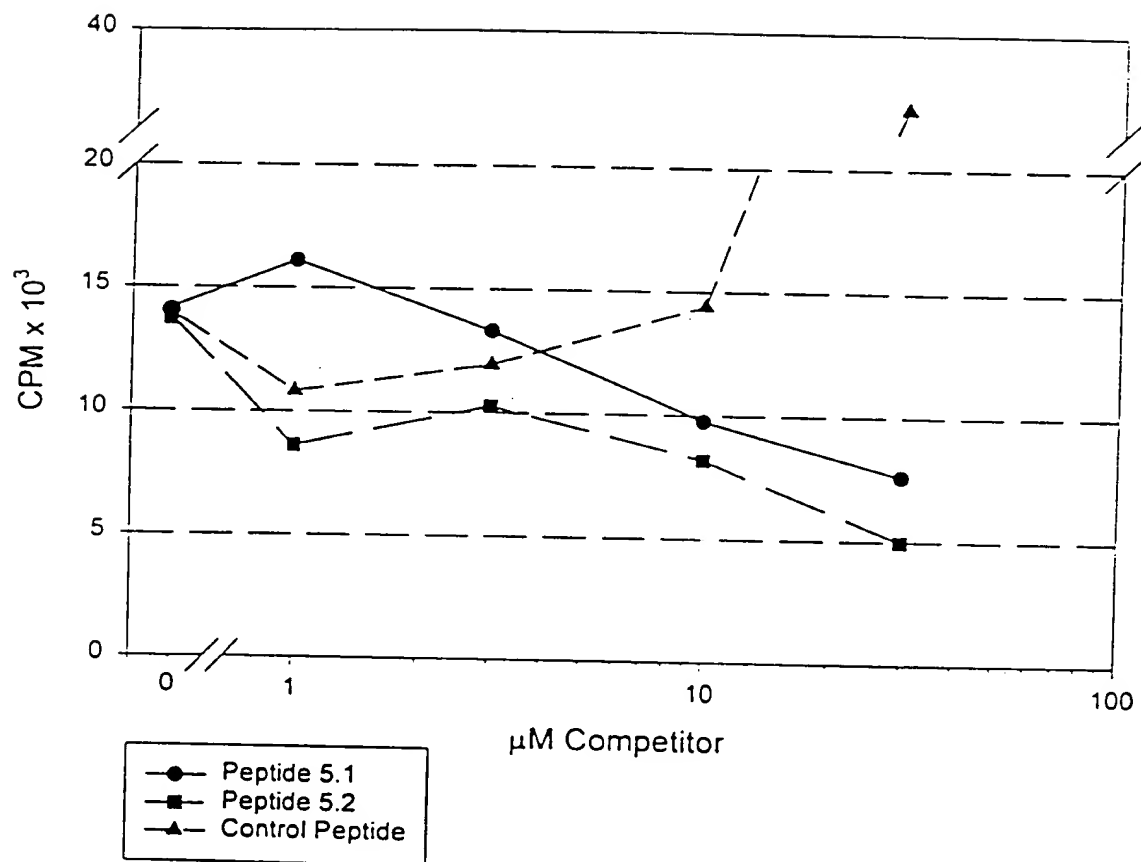


FIGURE 22

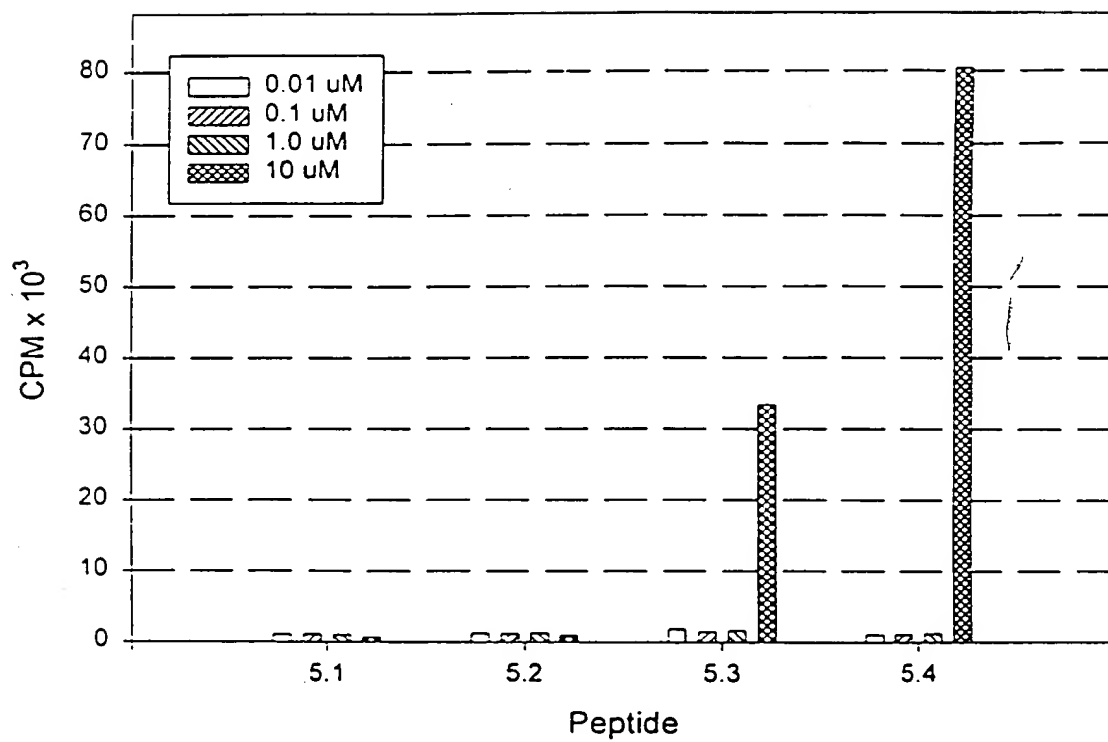


FIGURE 23

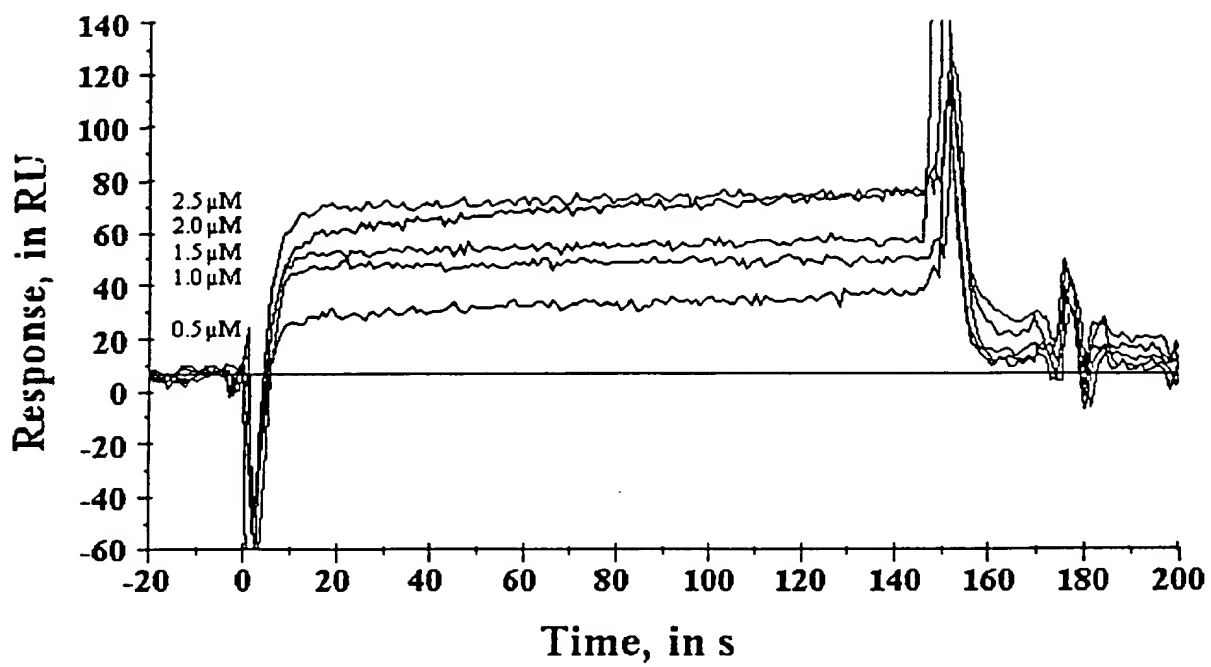


FIGURE 24A

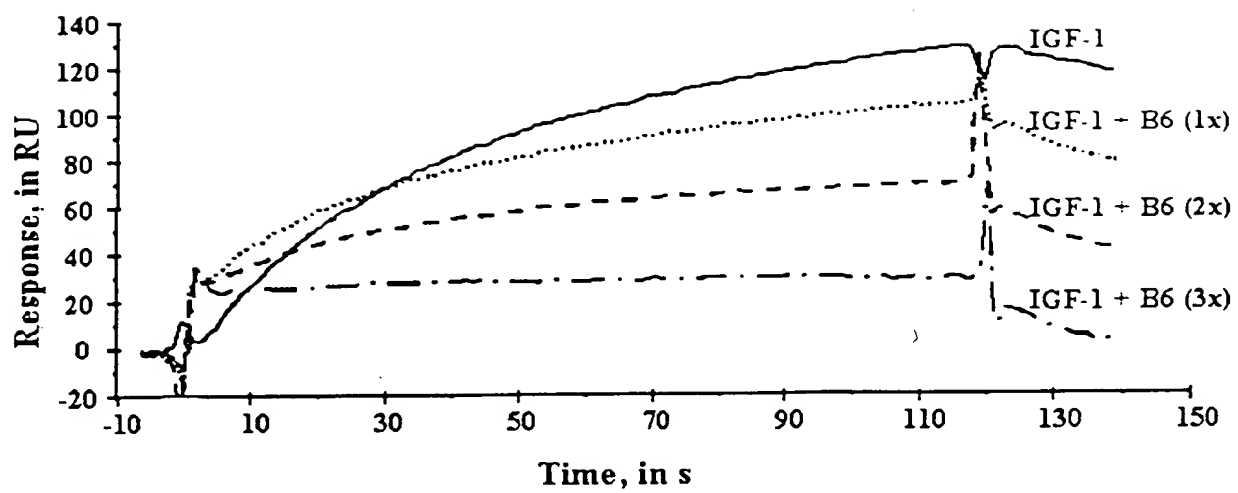


FIGURE 24B

GACTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACG
D Y K D D D D K Y R G M L V L G R I S D

GTGCTGGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAA

G A G K V A S E P P A R I G Q K V F A V N

CTTCTACGACTGGTTCGTTGCGGCCGCA 96 nt
F Y D W F V A A A

FIGURE 25A

CTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACGGTGCT
GGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAACTTCTACG
ACTGGTTCGTTGCGGCCGCAAGTGTGA 154 nt

FIGURE 25B

005252-222552

TTNNKNNKNNKNNK 21 aa
V X X X X

CTACAAAGACNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKA^{ACTTCT}ACGACTGGTTCGT^{TNNK}
NNKNNKNNKGCGGCCGCAGTGTGA

FIGURE 26B

2019年12月

Clone:

Binding Ratios:
Target E-Tag % Max

A6S-1-C5	DYKD	RIHNQTERCGNFYDWFVHqLV	AAA	7	27	26
A6S-1-G3	DYKD	VATVHVGGGMNFYDWFVAqVG	AAA	5	19	26
A6S-1-A2	DYKD	KDPVTVSQGRNFYDWFVVqIQ	AAA	5	20	25
A6S-1-D5	DYKD	RVGSGMEDLGNFYDWFVRQAq	AAA	5	25	20
A6S-1-H4	DYKD	HKSWTTMSPLNFYDWFVAqVE	AAA	3	18	17
A6S-2-F2	DYKD	LAMSVASRPANFYDWFVAqIV	AAA	30	35	86
A6S-2-D2	DYKD	RAERGSMDNSNFYDWFVqQLP	AAA	30	36	83
A6S-2-E3	DYKD	VqEGLSGMEGNFYDWFVDQLF	AAA	28	36	78
A6S-2-H2	DYKD	RGqRESDSGTNFYDWFVGAI R	AAA	28	40	70
A6S-2-A3	DYKD	SRAPYGSTAGNFYDWFVqAVS	AAA	25	37	68
A6S-2-H1	DYKD	RVGIqVDPHTNFYDWFVIQLT	AAA	27	42	64
A6S-2-F1	DYKD	VGqVGRYVRSNFYDWFVQqAM	AAA	8	30	27
A6S-2-G1	DYKD	RPqLVESGSKNFYDWFVqVVR	AAA	8	30	27
A6S-2-B2	DYKD	EMYGDTSERVNFYDWFVSALq	AAA	5	30	17
A6S-2-A1	DYKD	LSSRGRVTMRNFYDWFVAqVV	AAA	3	31	10
A6S-3-E10	DYKD	RVREKLPRPENFYDWFVNqIH	AAA	22	23	96
A6S-3-G2	DYKD	TWMWEERKqDNFYDWFVGQLK	AAA	20	21	95
A6S-3-E5	DYKD	RYRGERHDGRNFYDWFVEqVN	AAA	19	21	90
A6S-3-H2	DYKD	qGAEGRLSEGNFYDWFVQAVS	AAA	19	21	90
A6S-3-H9	DYKD	YSIEVqDWNENFYDWFVSQLG	AAA	20	23	87
A6S-3-G3	DYKD	PRLHMGSDMGDFYDWFVVqIA	AAA	18	21	86
A6S-3-F8	DYKD	GRGqGLKRPDnFYDWFVAAAK	AAA	20	25	80
A6S-3-G11	DYKD	GAVGLAEAGPNFYDWFVSqVq	AAA	19	24	79
A6S-3-H1	DYQD	PASNKNSLAENFYDWFVqQTR	AAA	23	30	77
A6S-3-E6	DYKD	DARDHGVVMSNFYDWFVAqVS	AAA	5	20	25
A6S-3-D9	DYKD	SLOGADFqQGNFYDWFVSELA	AAA	4	17	24
A6S-3-E3	DYKD	RPSLPEVRPGNFYDWFVqSVR	AAA	4	19	21
A6S-3-H8	DYKD	NPTSVqQYGVNFYDWFVNVLS	AAA	4	20	20
A6S-3-G4	DYKD	CADPGACSSLNFYDWFVqMRG	AAA	4	21	19
A6S-3-B10	DYKD	YDqDPPYWGLNFYDWFVREVA	AAA	3	16	19
A6S-3-C1	DYKD	RPVIGGGGTRNFYDWFVAqMI	AAA	3	17	18
A6S-4-G5	DYKD	QEVTRTRDDKNFYDWFVSqIF	AAA	26	18	144
A6S-4-D2	DYKD	PPYRSSRLGENFYDWFVMqVR	AAA	26	19	143
A6S-4-F6	DYKD	LKGSSQPLSVNFYDWFVQQIK	AAA	24	17	142
A6S-4-H4	DYKD	PRMVEKPSEDNFYDWFVTqLS	AAA	28	20	141
A6S-4-C1	DYKD	CWARPCGDAANFYDWFVqQAS	AAA	22	16	141
A6S-4-G3	DYKD	GAQAIREIHNFYDWFVAQVT	AAA	29	21	139
A6S-4-H3	DYKD	GRGDQRHETTnFYDWFVRELq	AAA	28	20	137

FIGURE 28

A6S-4-H6.	DYKD	GSIAQLIMRANFYDWFVEqTN	AAA	24	18	130
A6S-4-G6	DYKD	RLMGGIAEPqNFYDWFVREVA	AAA	25	20	126
A6S-4-H5	DYKD	HHSPGNEHGYNFYDWFVLqVA	AAA	24	19	123
A6S-4-E4.	DYKD	ERSAAGFREGNFYDWFVAqVN	AAA	32	27	120
A6S-4-F5.	DYKD	GSQHSGREPHNFYDWFVAqVG	AAA	28	24	120
A6S-4-D4	DYKD	IARMRETFQPNFYDWFVDQLA	AAA	21	18	118
A6S-4-C6	DYKD	RLDRSSTSGVNFYDWFVAqVG	AAA	28	25	116
A6S-4-D3	DYKD	GLRSEQGNRLNFYDWFVAQIA	AAA	23	20	116
A6S-4-F2	DYKD	SVIQTRQDETNFYDWFV?AMS	AAA	26	23	115
A6S-4-A5	DYKD	VEVQRHIRKDNFYDWFVKQID	AAA	22	19	115
A6S-4-C3	DYKD	VTMLDKGAQDNFYDWFVREVA	AAA	24	21	114
A6S-4-F3	DYKD	HNSSSPMRTGNFYDWFVQELR	AAA	30	26	113
A6S-4-B4	DYKD	ERSPRPALASNFYDWFVQQVV	AAA	21	19	113
A6S-4-B6	DYKD	SDARQAGLQENFYDWFVSQVR	AAA	26	23	113
A6S-4-B1	DYKD	RHERGKEGPGNFYDWFVSQVV	AAA	21	19	112
A6S-4-G4	DYKD	SALSGPVqPINFYDWFVTGM	AAA	30	26	112
A6S-4-A6	DYKD	HVEHMAVGdGNFYDWFVqLR	AAA	23	21	111
A6S-4-F4	DYKD	VGHSGVPPYPNFYDWFVMQVS	AAA	24	22	110
A6S-4-D6	DYKD	LGAAETWDGINFYDWFVKQVS	AAA	24	22	110
A6S-4-E6	DYKD	RSSGGLLSqGNFYDWFVSQLE	AAA	26	24	109
A6S-4-A3	DYKD	LAINDLVTHKNFYDWFVDQLR	AAA	20	18	109
A6S-4-E3	DYKD	RGMTGMVGRGNFYDWFVGQLR	AAA	23	21	109
A6S-4-A2	DYKD	IGGQGQHdGNFYDWFVEALA	AAA	22	20	107
A6S-4-B2	DYKD	QSVDLSRPDSNFYDWFVEVLS	AAA	22	21	105
A6S-4-H2	DYKD	VTFTSAVFHENFYDWFVRQVS	AAA	20	19	104
A6S-4-D1	DYKD	SNPSRQDASVNFYDWFVREVA	AAA	22	22	103
A6S-4-H1	DYKD	IVAGARHSEVNFYDWFVIQVR	AAA	18	18	102
A6S-4-E2	DYKD	?DGQSVSSKGNFYDWFVQqMT	AAA	25	25	101
A6S-4-G1	DYKD	AELVGAGVRGNFYDWFVDQLV	AAA	16	16	101
A6S-4-G2	DHKG	SAGHHMPRESNFYDWFVDQVV	AAA	24	25	99
A6S-4-A1.	DYKD	DSSRLWLGERNFYDWFVAqIS	AAA	12	17	68

FIGURE 28 (Cont.)

Name	Sequence	#Found	Ratio	IGF Inh.	GHR*
H5:	LCQSLGVTPGWLAGWCA	-	1.2	-	2.0
2C3:	VCQRLGGTFPGWLVGVC	-	1.1	-	1.1
JBA5:	LCQSWGVRI-GWLAGLCP	19	~24.0	~45%	1.2
E2A12:	LCQSLGFTDLDWLACWFE	10	~17.5	~54	1.1
E1A11:	VCQSLGITDLGLCAGWGA	1	16.4	50	1.0
E4B10:	LCQSLGLTHPGFEAWLCA	5	~11.7	~50	1.2
E4C10:	LCQNFQVTDPGCFYGWFA	1	9.9	~51	0.7
E4A9:	LCQSSGLSFLGCL-GWWA	14	~8.5	~65	1.0
JBB6:	PCQRLGDTHLCWLAGWFA	6	~8.3	~65	1.1
E1F9	PCQSLGLTCSGWFEWGA	1	8.3	68	1.2
E4G7:	QWQSLGVTCPGSWAELCA	1	6.0	50	1.3
E4A11:	LWQSVGIKYPGGLAGWLA	1	5.8	67	1.4
E1B9:	LCQSLGVTYWEGWLAWLCA	3	5.5	60	1.1
E4A12:	VCQGLGVECPGWFAWWA	3	~5.3	~55	1.2
E4F11:	LCQGWGIRI-GWLVGRCM	1	2.7	58	1.1
E1D3:	LCQSLGVTPGWLAGGCA	1	2.0*	-	1.0

FIGURE 29

Genomic rVab Library

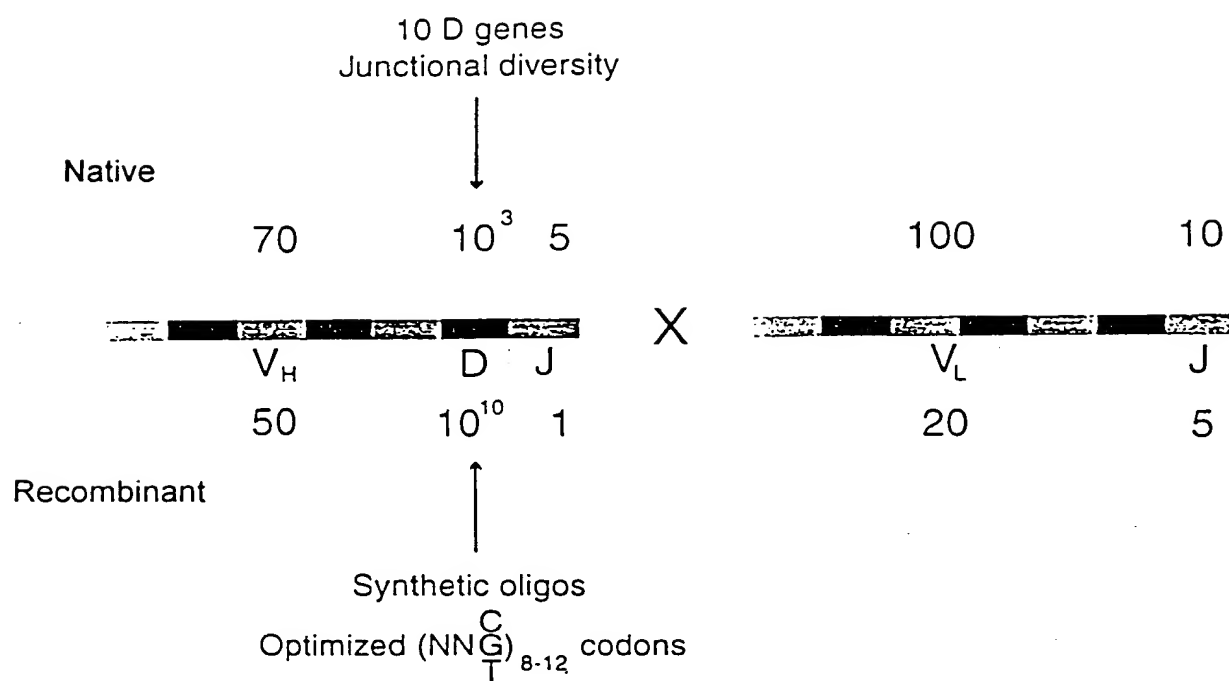


FIGURE 30

VH Gene Sequences

DP-1
DP-10
DP-12
DP-14
DP-15
DP-2
DP-21
DP-25
DP-29
DP-30
DP-31
DP-32
DP-33
DP-35
DP-38
DP-39
DP-40
DP-42
DP-44
DP-45
DP-46
DP-47
DP-5
DP-50
DP-51
DP-52
DP-53
DP-54
DP-59
DP-63
DP-66
DP-67
DP-68
DP-69
DP-7
DP-70
DP-71
DP-73
DP-74
DP-8
hv1263
VHD26

Lambda and Kappa Gene Sequences

DPK11
DPK15
DPK18
DPK2/L14+
DPK3/L11+
DPK4
DPK6
DPK8/Vd+
DPL23
HK101
L22+
L23/L23a
LFVK431
VA++

FIGURE 31

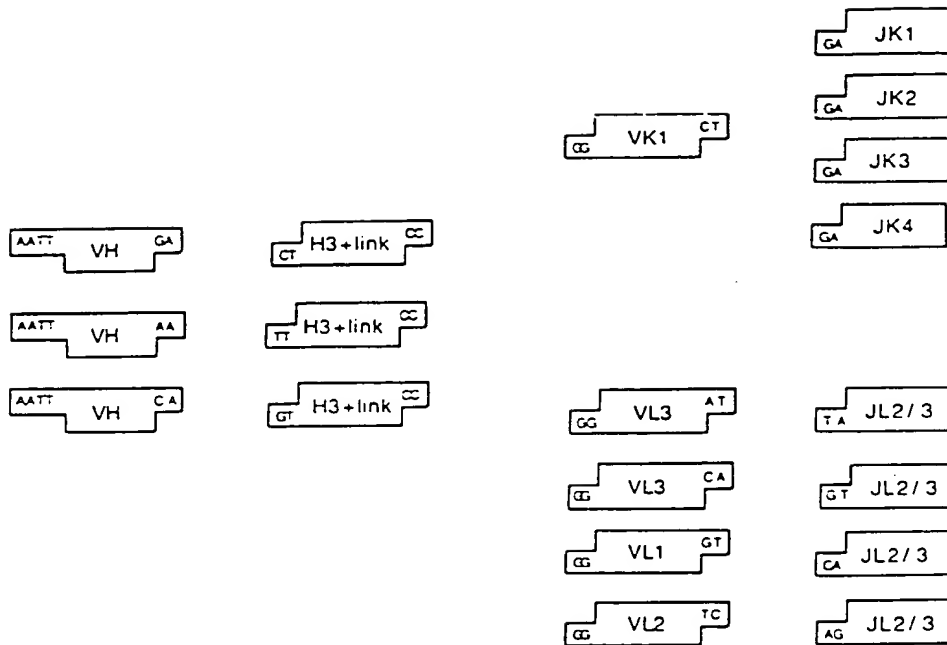


FIGURE 32

EcoRI / SfiI / VII gene / CDR III / JHb gene / G4S linker
 CCGGAATTTCGGCCAGCCGCGCCNNH-----HAA
 GGCCTTAAGCCGGTCCGCGCCNNH-----N
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49
 CTHHV---HNVACCCCGCTCCCTTGGACACAGTGGCAGAGAGTCCACCTCCGCCCAAGTCCGCCCTCCACCGACCGCCACCGCCTA
 BamHI

CCGCAATTTCGGCCAGCCGCGCCNNH-----HAA
 GGCCTTAAGCCGGTCCGCGCCNNH-----N
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49

CCGCAATTTCGGCCAGCCGCGCCNNH-----HAA
 GGCCTTAAGCCGGTCCGCGCCNNH-----N
 3' end for 4 VII genes: DP2, DP3, DP5 and DP38

All kappa genes:
 Asp Pro
 NNN-----CCT
 GGNH-----G
 (except VK L20)

JK1 gene / NotI / PCR primer site /
 TrpThrPheGlyGlnGlyThrLysValGluLeuLys
 TCGACGTTTCGGCCAGCCGCGCCNNH-----HAA
 GAACCTCCAGCCGGTCCCTCGTCCACCTTTAGTTTCGGCGGCTCACACTCAGGTTTCTTAAGC

JK2 gene /
 TyrThrPheGlyGlnGlyThrLysValGluLeuLys
 TACACTTTTCGGCCAGCCGCGCCNNH-----HAA
 GAATGTCAGAACCGGTCCTCGTTCGACCTCTAGTTT

JK3 gene /
 PheThrPheGlyProGlyThrLysValAspLeuLys
 TTCACTTTTCGGCCAGCCGCGCCNNH-----HAA
 GAAAGTCAGAACCGGTCCTCGTTCGACCTCTAGTTT

DPL16 (=v3s1)+
 Lambda 3 genes: / +v318 /
 Ser His
 NNN-----CAT
 GGNH-----G
 / JL2/3 for DPL16+v3s1+v318 / NotI / PCR primer site /
 ValValPheGlyGlyGlnGlyThrLysLeuThrValLeu
 GTGGTATTCGGCGGAGGACCAAGCTGACCGCTCTAGCGCGCGCCAGTGTGAGTCCAAAAGATTTTCG
 TACACCATAGCCCGCTCCCTCGTTCGACTGGCAGGATCCGCCGCTCACACTCAGGTTTCTTAAGC

Lambda 3 gene: /DPL23 (=VL3.11)/
 Ser Ala
 NNN-----GCA
 GGNH-----C
 for DPL23+VL3.1
 GTG--- continued as for JL2/3
 GTCAC---

Lambda 1 genes: / DPL2+DPL3 /
 Gln Gly
 NNN-----GGT
 GGNH-----C
 for DPL2+DPL3
 GTG--- continued as for JL2/3
 CACAC---

Lambda 2 gene: / DPL11 /
 Gln Leu
 NNN-----CTC
 GGNH-----G
 for DPL11
 GTG--- continued as for JL2/3
 AGCAC---

FIGURE 33

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GGTGCAGCTG	GTCGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	V Q L	V E S G	G G L	V K P	
GGGGGICCC	TTAGACTCTC	CTGTGCAGCC	TCGTGATCA	CTTTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACAACAGA	CTACGCTGCA	CCCGTGAAG	GCAGATTCAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACACGCT	GTATCTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTCATTACT	GTACCACAGT	TGCGTTGTCT	GCCGACCGTG	GGATGTGGGG	TCAAGGAACT	360
V Y Y C	T T V	A L S	A D R G	M W G	Q G T	
CTGGTCACCG	TCTCTCAGG	TGGAGGCGGT	TCAGGCGGAG	GTGGCTCTGG	CGGTGGCGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGATGTTG	TGATGACTCA	GTCTCCACTC	TCCCTGCCCC	TCACCCCTTG	ACAGCCCGCC	480
S D V V	M T Q	S P L	S L P V	T L G	Q P A	
TCCATCTCCT	GCAGGTCTAG	TCAAAGCCTC	GTATACAGTG	ATGGAAACAC	CTACTTGAAT	540
S I S C	R S S	Q S L	V Y S D	G N T	Y L N	
TGGTTTCAGC	AGAGGCCAGG	CCAATCTCCA	AGGCGCCTAA	TTTATAAGGT	TTCTAACCGG	600
W F Q Q	R P G	Q S P	R R L I	Y K V	S N R	
GACTCTGGGG	TCCCAGACAG	ATTCAGCGGC	AGTGGGTCAG	GCACTGATTT	CACACTGAAA	660
D S G V	P D R	F S G	S G S G	T D F	T L K	
ATCAGCAAGG	TGGAGGCTGA	GGATGTTGGG	GTTTATTACT	GCATGCAAGG	TACACACTGG	720
I S R V	E A E	D V G	V Y Y C	M Q G	T H W	
CCTTACACTT	TTGGCCAGGG	GACCAAGCTG	GAGATCAAAG	CGGCGGC		767
P Y T F	G Q G	T K L	E I K			

FIGURE 34

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GATGCAGCTG	GTCGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCGCGATICA	CITTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACAACAGA	CTACGCTGCA	CCCGTGAAAG	GCAGATTAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACAGCCT	GTATCTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTGTATTACT	GTACCACATG	GGGCTCCGTC	GACACGGACA	ACTACGCCAG	GTTTTGGGGT	360
V Y Y C	T T W	G S V	D T D N	Y A R	F W G	
CAAGGAACTC	TGGTCACCGT	CTCCTCAGGT	GGAGGGCGTT	CAGGCGGAGG	TGGCTCTGGC	420
Q G T L	V T V	S S G	G G G S	G G G	G S G	
GGTGGCGGAT	CCGACATCCA	GATGACCCAG	TCTCCATCCT	CCCTGTCTGC	ATCTGTAGGA	480
G G G S	D I Q	M T Q	S P S S	L S A	S V G	
GACAGAGTCA	CCATCACTTG	CCGGGGGAGT	CAAGGGCATTA	GCAATTATTT	AGCCTGGTAT	540
D R V T	I T C	R A S	Q G I S	N Y L	A W Y	
CAGCAGAAC	CAGGGAAAGT	TCCTAAGCTC	CTGATCTATG	CTGCATCCAC	TTTGCAATCA	600
Q Q K P	G K V	P K L	L I Y A	A S T	L Q S	
GGGGTCCCAT	CTCGGTTTCAG	TGGCAGTGGG	TCTGGGACAG	ATTTCACTCT	CACCATCAGC	660
G V P S	R F S	G S G	S G T D	F T L	T I S	
AGCCTGCAGC	CTGAAGATGT	TGCAACTTAT	TACTGTCAAA	AGTATAACAG	TGCCCCCTCTC	720
S L Q P	E D V	A T Y	Y C Q K	Y N S	A P L	
ACTTTTCGGCG	GAGGGACCAA	GGTGGAGATC	AAAGCGGCGC	C		761
T F G G	G T K	V E I	K			

4

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GATGCAGCTG	GTTGGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CTTTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACAAACAG	CTACGCTGCA	CCCGTGAAAG	GCAGATTAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACACGCT	GATCTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTTGATTACT	GTAACACACC	GGGCTGGTAT	GGGGCCGAGG	ATAAGTGGGG	TCAAGGAACT	360
V Y Y C	T T P	G W Y	G A E D	K W G	Q G T	
CTGGTCACCG	TCTCCTCAGG	TGGAGGCGGT	TCAGGGGGAG	GTGGCTCTGG	CGGTGGGGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGACATCC	AGATGACCCA	GCTCCATCC	TCCCTGTCTG	CATCTGTAGG	AGACAGAGTC	480
S D I Q	M T Q	S P S	S L S A	S V G	D R V	
ACCATCACTT	GGCGGGCGAG	TCAGGGCAAT	AGCAATTATT	TAGCCTGGTA	TCAGCAGAAA	540
T I T C	R A S	Q G I	S N Y L	A W Y	Q Q K	
CCAGGGAAAG	TTCTTAGGCT	CCTGATCTAT	GCTGCATCCA	CTTTGCAATC	AGGGGTCCCA	600
P G K V	P K L	L I Y	A A S T	L Q S	G V P	
TCTCGGTTCA	GTGGCAGTGG	ATCTGGGACA	GATTTCACTC	TCACCATCAG	CAGCCTGCAG	660
S R F S	G S G	S G T	D F T L	T I S	S L Q	
CCTGAAGATG	TTGCAACTTA	TTACTGTCAA	AAGTATAACA	GTGCCCCCTT	CACCTTTCGGC	720
P E D V	A T Y	Y C Q	K Y N S	A P F	T F G	
CCTGGGACCA	AAGTGGATAT	CAAAGCGGCC	GC			752
P G T K	V D I K					

006360 0000000000

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTACAGCCT	60
	Q	V Q L	V E S G	G G L	V Q P	
GGGGAATCCC	TGAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CCATCAGTAA	CAGTGACATG	120
G G S L	R L S	C A A	S G F T	F S N	S D M	
AAGTGGGTCC	ATCAGGCTCC	AGGAAAGGGG	CTGGAGTGGG	TATCGGGTGT	TAGTTGGAAT	180
N W V H	Q A P	G K G	L E W V	S G V	S W N	
GGCAGTAGGA	CGCACTATGC	AGACTCTGTG	AAGGGCCGAT	TCATCATCTC	CAGAGACAAT	240
G S R T	H Y A	D S V	K G R F	I I S	R D N	
TCCAGGAACA	CCCTGTATCT	GCAACGAAT	AGCCTCAGGG	CCGAGGACAC	GGCTGTGTAT	300
S R N T	L Y L	Q T N	S L R A	E D T	A V Y	
TACTGTGTGA	GAAACGATGG	CGAGTGGTAC	GGGGCTGGG	GTCAAGGAAC	TCTGGTCACC	360
Y C V R	T D G	E W Y	G A W G	Q G T	L V T	
GTCTCTCAG	GTGGAGGCGG	TTACAGGCGA	GGTGGCTCTG	GGGTGGGGG	ATCCGCCATC	420
V S S G	G G G	S G G	G G S G	G G G	S A I	
CAGATGACCC	AGTCTCCATC	CTCCCTGTCT	GCATCTGTAG	GAGACAGAGT	CACCATCACT	480
Q M T Q	S P S	S L S	A S V G	D R V	T I T	
TGCCCCGCA	GTACAGGCAT	TAGAATGAT	TTAGGCTGGT	ATCAGCAGAA	ACCAGGGCAA	540
C R A S	Q G I	R N D	L G W Y	Q Q K	P G K	
GGCCCTAAGC	TCCGGATCTA	TGCTGCATCC	AGTTTACAAA	GTGGGGTCCC	ATCAAGGTTT	600
A P K L	R I Y	A A S	S L Q S	G V P	S R F	
AGCGGCAGTG	GATCTGGCAC	AGATTTCACT	CTCACCATCA	GCAGCCTGCA	GCCTGAAGAT	660
S G S G	S G T	D F T	L T I S	S L Q	P E D	
TTTGCAACTT	ATTACTGTCT	ACAAGATTAC	AATTACCCCTC	TCACTTTCCG	CGGAGGGACC	720
F A T Y	Y C L	Q D Y	N Y P L	T F G	G G T	
AAGGTGGAGA	TCAAAGCGGC	CGC				743
K V E I	K					

FIGURE 37

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGCCAGGCGG	CCATGCCCCA	GATGCAGCTG	GTGCGAGTCTG	GGGGAGGCTT	GGTACAGCCT
	Q	M Q L	V Q S G	G G L	V Q P
GGGGGGTCCC	TGAGACTCTC	CTGTGCAGGC	TCTGGATTCA	OCTTCAGTAG	CTATGCTAIG
G G S L	R L S	C A G	S G F T	F S S	Y A M
CACTGGGTTC	GCCAGGCTCC	AGGAAAAGGT	CTGGAGTGGG	TATCAGCTAT	TGGTACTGGT
H W V R	Q A P	G K G	L E W V	S A I	G T G
GGTGGCACAT	ACTATGCAGA	CTCCGTGAAG	GGCCGATTCA	CCATCTCCAG	AGACAATGCC
G G T Y	Y A D	S V K	G R F T	I S R	D N A
AAGAATCCT	TGTATCTTCA	AATGAACAGC	CTGAGAGCCG	AGGACATGGC	TGTGTATTAC
K N S L	Y L Q	M N S	L R A E	D M A	V Y Y
TGTGCAAGAG	AGGGCGAGCT	CGGGGTGACC	TCCTTCTGGG	GTCAAGGAAC	TCTGGTCACC
C A R E	G E L	G V T	S F W G	Q G T	L V T
GTCTCCTCAG	GTGGAGGGGG	TTCAGGGCGA	GGTGGCTCTG	GCGGTGGGGG	ATCCGACATC
V S S G	G G G	S G G	G G S G	G G G	S D I
CAGATGACCC	AGTCTCCATC	CTCCCTGTCT	GCATCTGTAG	GAGACAGAGT	CACCATCACT
Q M T Q	S P S	S L S	A S V G	D R V	T I T
TGCCGGGGCA	GTCAGGGCAT	TAGCAATTAT	TTAGCCTGGT	ATCAGCAGAA	ACCAGGGAAA
C R A S	Q G I	S N Y	L A W Y	Q Q K	P G K
GTTCCTAAGC	TCCTGATCTA	TGCTGCATCC	ACTTTGCAAT	CAGGGGTCCC	ATCTCGGTTC
V P K L	L I Y	A A S	T L Q S	G V P	S R F
AGTGGCAGTG	GATCTGGGAC	AGATTTCACT	CTCACCATCA	GCAGCCTGCA	GCCTGAAGAT
S G S G	S G T	D F T	L T I S	S L Q	P E D
GTTCGAACTT	ATTACTGTCA	AAAGTATAAC	AGTGGCCCCT	GGACGTTCCG	CCAAGGGACC
V A T Y	Y C Q	K Y N	S A P W	T F G	Q G T
AAGGTGGAAA	TCAAAGCGGC	CGC			
K V E I K					

FIGURE 39

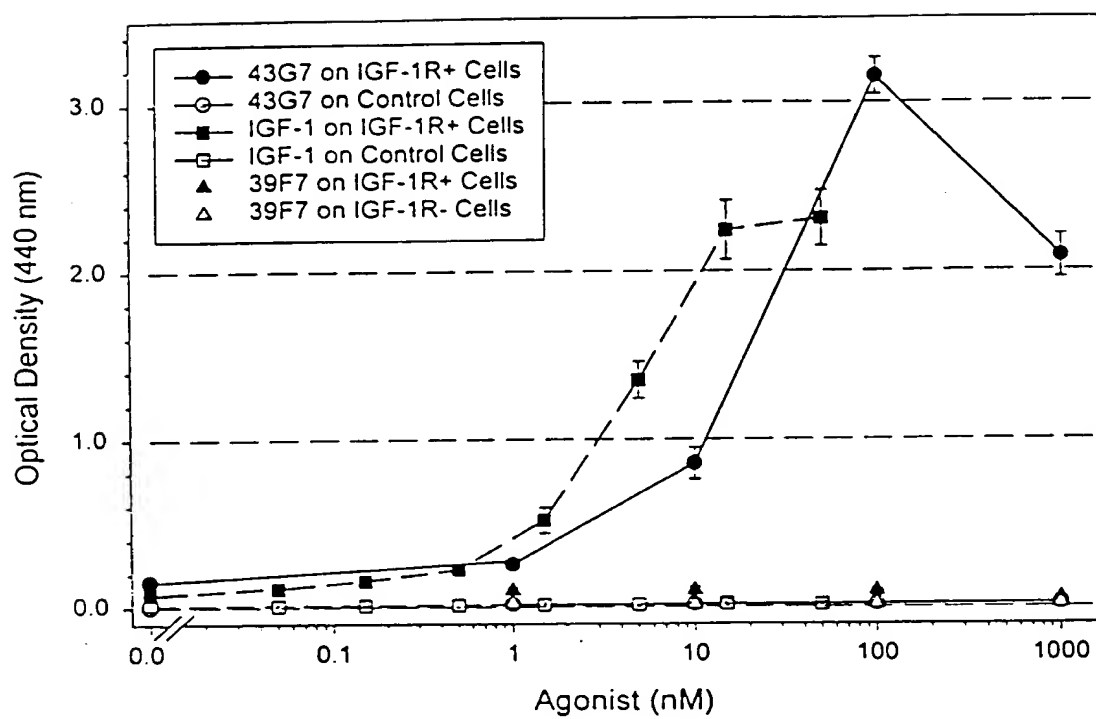


FIGURE 41

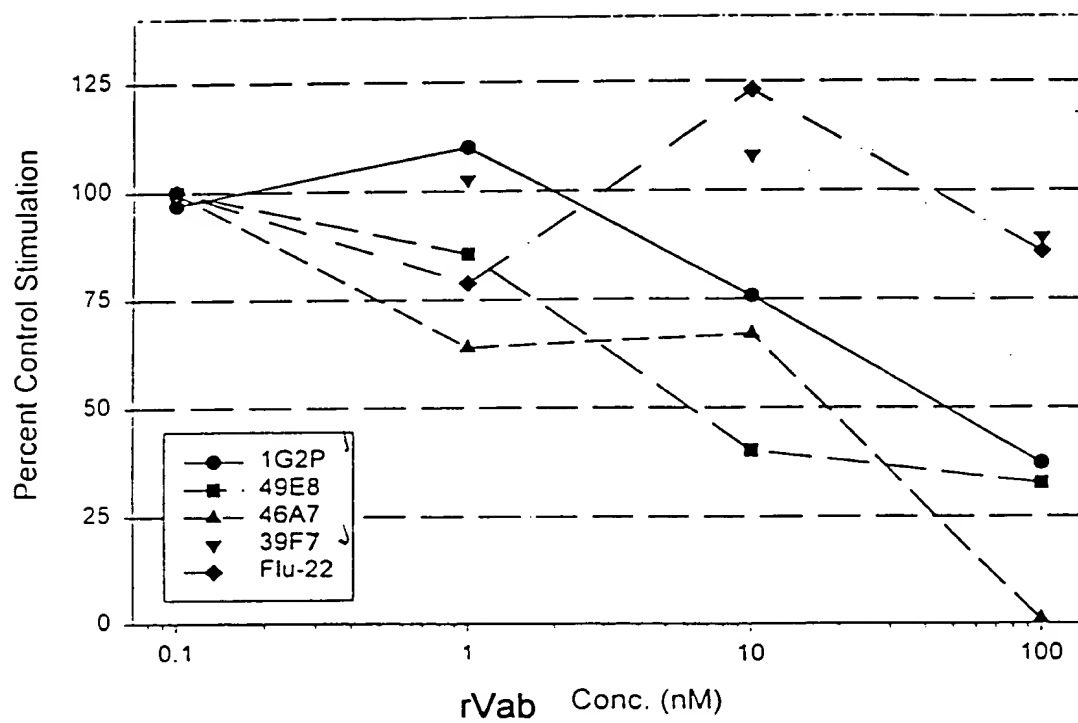


FIGURE 42

Figure 1 is a line graph showing the effect of IGF-1 concentration on B6 specific binding. The y-axis represents 'B6 Specific Binding (% Control)' and ranges from 0 to 100. The x-axis represents '[IGF-1], uM' on a logarithmic scale, with major ticks at 0, 0.1, 1, 10, and 100. The data points are connected by a solid line, showing a dose-dependent decrease in binding as IGF-1 concentration increases.

[IGF-1], uM	B6 Specific Binding (% Control)
0	100
0.03	88
0.1	84
0.3	45
1	43
3	24
10	9
30	4
100	0

FIGURE 43

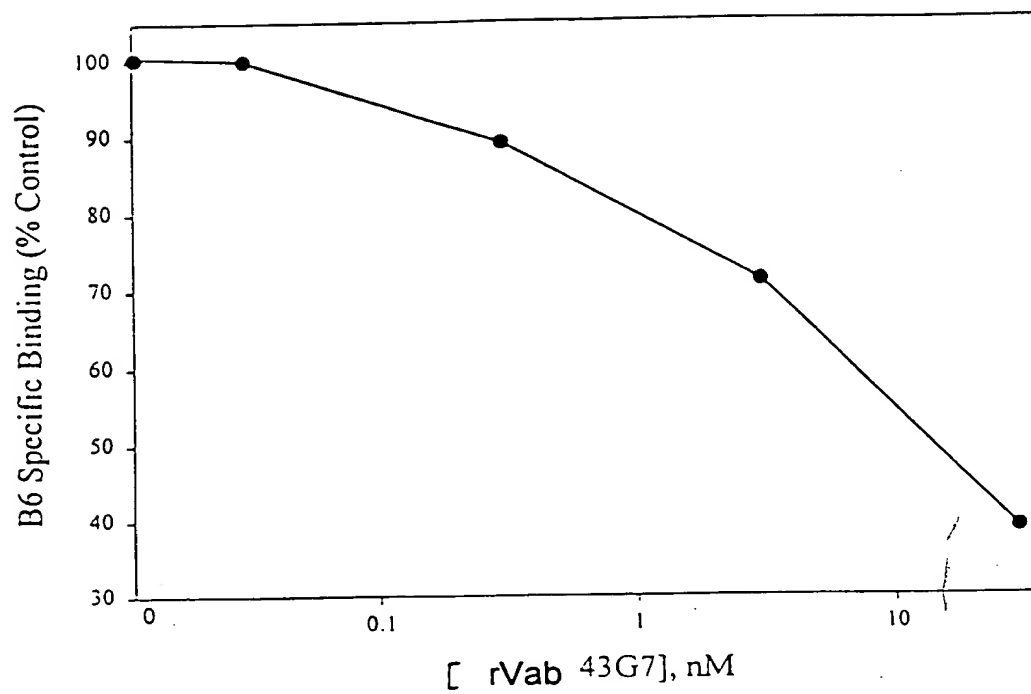


FIGURE 45

FIGURE 46A

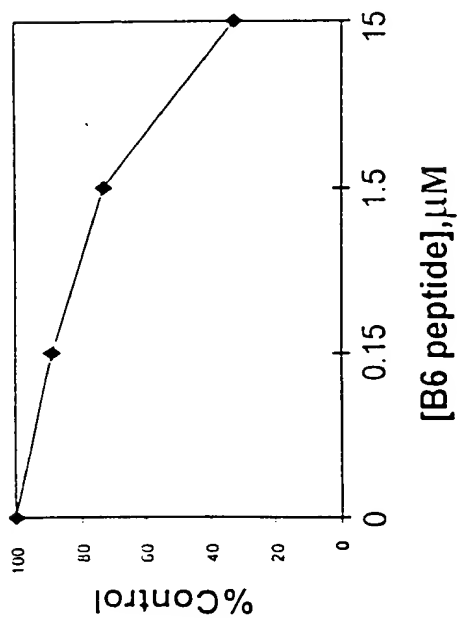


FIGURE 46B

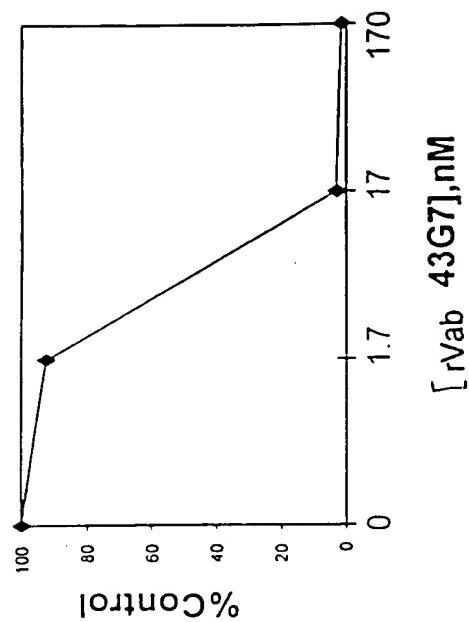


FIGURE 46C

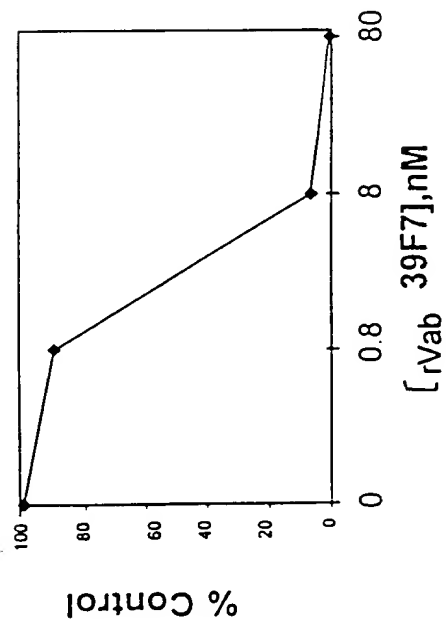
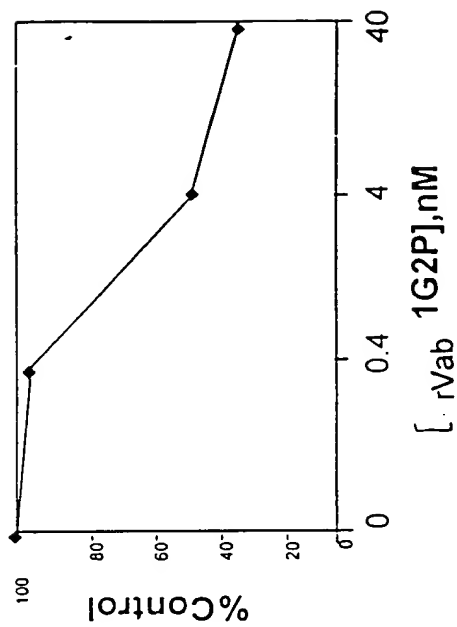


FIGURE 46D



Group 1: Formula 1 Motif

		Found	IR	IGF
20D3*	IGGGQHQDGNFYDWFVEALA	18	+	+++
20F1	VFWNCRSQQLDEYEFWEQAA	16	+	+++
G3	RGGTIFYEFWESALRRKHGAG	8	+	+++
20H1	RVAGAISAPGLVSNKQDGLFYSWRE	5	+	+++
20D1*	VLQARIIGCDSDVDCFYEWFA	4	+	+++
D2	DPERMQSDVGFYEFWFRAAVG	3	+	+++
B8	WSALLSVMDTGFYAWEDDAV	2	++	+++
C4	DIGSDGHGRRWDSFYRWFEEM	2	+	+++
A8	IGGSFVEFYGFENDQV	2	+	+++
E7	GHSWALVRHVDRRLFYEWFDL	1	++	+++
C8	LPAGGAQGFVVRGFYEFWEES	1	+	+++
H8	RDKPTDQEEQNWSFYEFWRH	1	+	+++
E2	SRDQTNFTFNSAGFYGFWEER	1	+	+++
B12	GAFYRWTFHEALVGSERVPDV	1	+	+++
D10-2	RIGGGWARSEGEFYEFVREL	1	+	++
G8	RMEYEFWFSQMGAGPTEGSA	1	+	++
H3	HEAFYDWFSAALVDGGYELMG	1	+	++
3G11	FYGFWSRQLSLTPRDDWGLP	1	+	++
F4	GVGTLTMSSDAFYTWTV	1	+	++
E7-2	LGTSAGQGVGHRAFYQWFQS	1	+	+
40G11	-----AALDRLFYSWFS	3	+	+++
40R2	IRDMHYVWVQDRDRYINCVRQWYISDRYNPGSAFYRWFD	2	+	++
40B12	RMGLQALAHYRKSA-----GPIFLSSGSVIKSGEDPFYAWFRLO	1	+	++

FIGURE 47

Group 2: Formula 6 Motif

20A4* EIEAEWGRVRCIVYGRGVGG
DS WLDQEWANWVQCIVYGRGCP

Target	
Found	IR IGF
13	+++ 0
3	+++ ?

Group 3: Formula 2 Motif

20E2 DYKDFYDAIDQLVRGSARAGTRD
20C11 DYKDDRAFYNGLRDLVGAVYGAWD
20A12 DYKDRIFYCGIQALGANLGYSGCV
C6 DYKDFYSALWGLCGVTGCG
A6 RGQSDAFYSGGLWALIGLSDG

Target	
Found	IR IGF
1	+ +++++
1	+ +++++
1	+ +++++
1	+ +++++
1	+ +++++

Group 5: Miscellaneous Motif 10

D0.2 PFGGGRWVGIPRMWYRNS
114 WWWGGRNRWWLERWGLGGER

Target	
Found	IR IGF
1	++ ++
1	+ +

Group 4 and 6: Miscellaneous Motif 10

D10 LGPLLRWGSSEVCGVWPDCE
F2 SMFVAGSDRWPGYGYLADWL
F8 VRGFQGGTVWPGYEWLRNAA
A2 CRVALNGFVWPRWMSRPV
A4 WPGYLEFEALQDWRGSTD

Target	
Found	IR IGF
3	++ 0
1	++ ++
1	++ ?
1	++ +
1	0 +++

Group 7: Formula 4 Motif

F8 HLCVLEELFWGASLFGYCSG
B6 ACSSEFVKPGEGLQCLGSI
40D6 PERGRLRTAMQIMRRPRDWHIFPHSLFWGAPPLSG

Target	
Found	IR IGF
4	+++ +
1	0 ++
1	0 0

**Group 8: Non-Aligning
Miscellaneous
Sequences**

FIGURE 49A

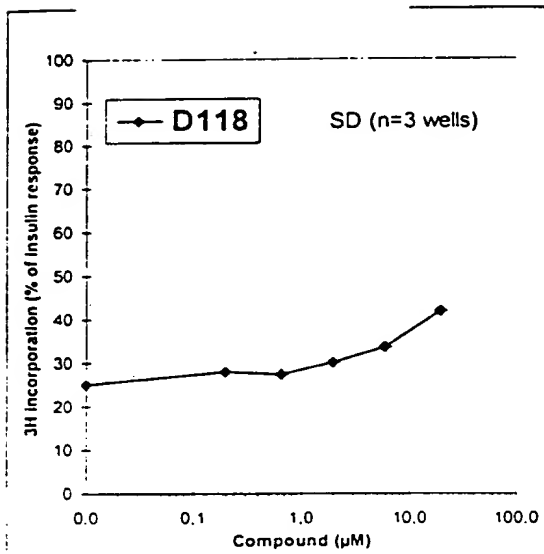


FIGURE 49B

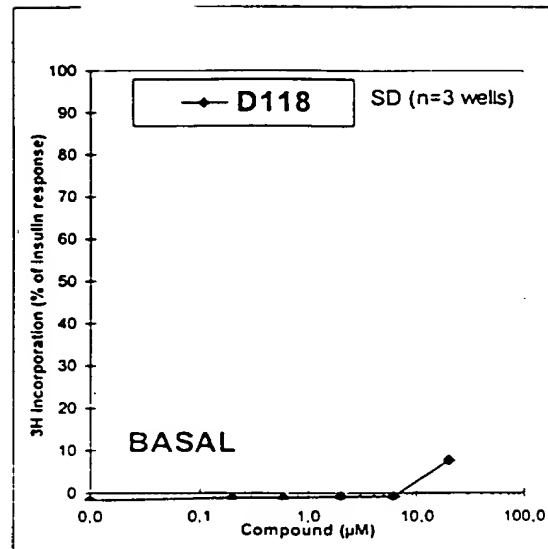


FIGURE 49C

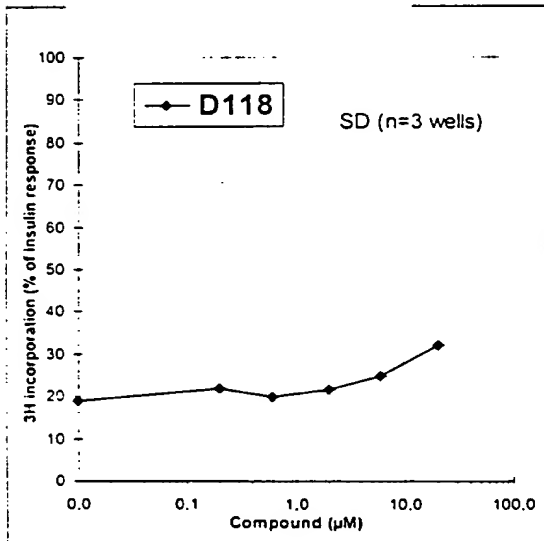


FIGURE 49D

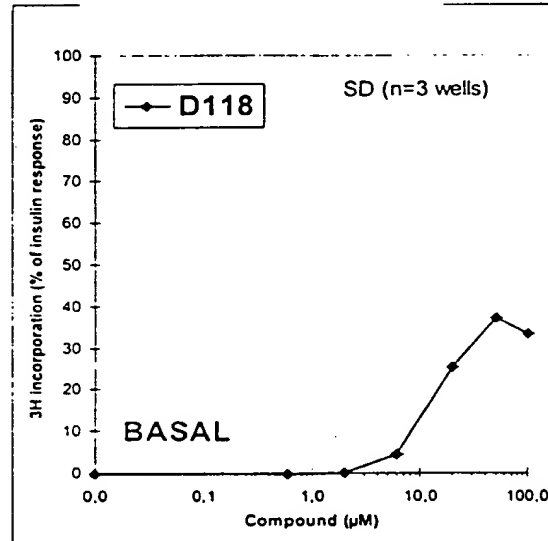


FIGURE 50A

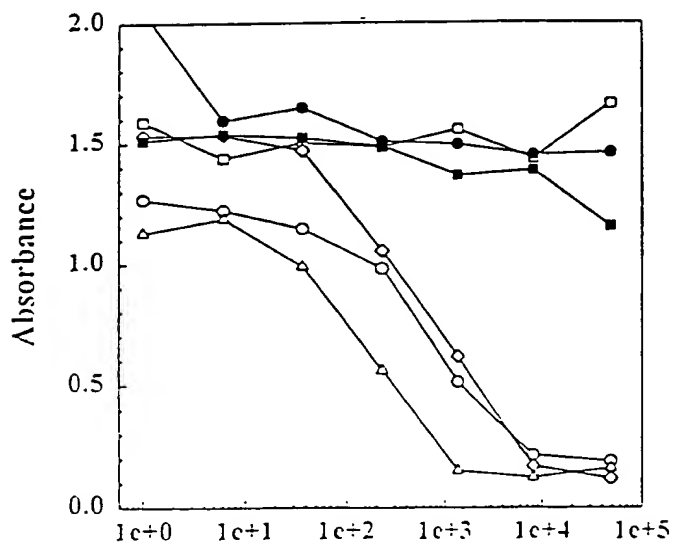


FIGURE 50B

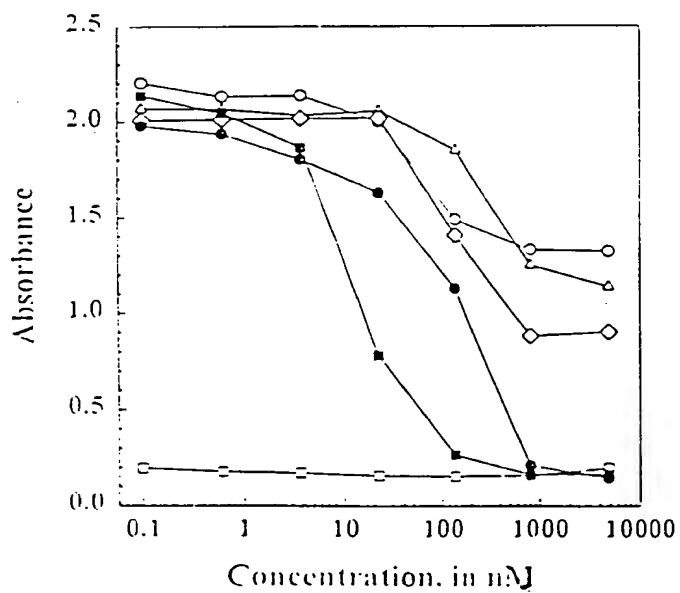
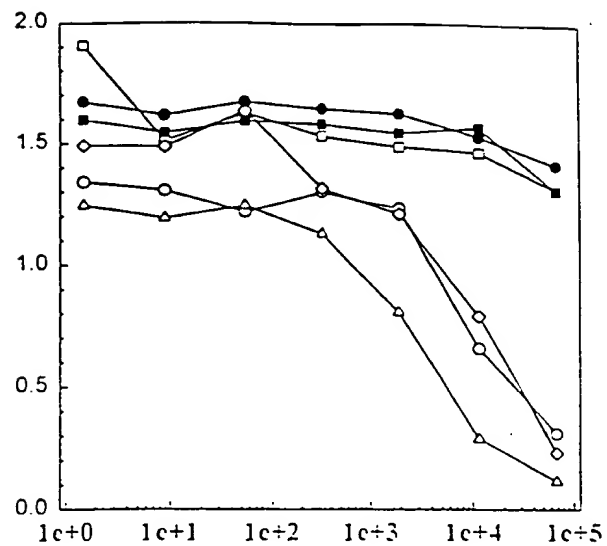


FIGURE 50C

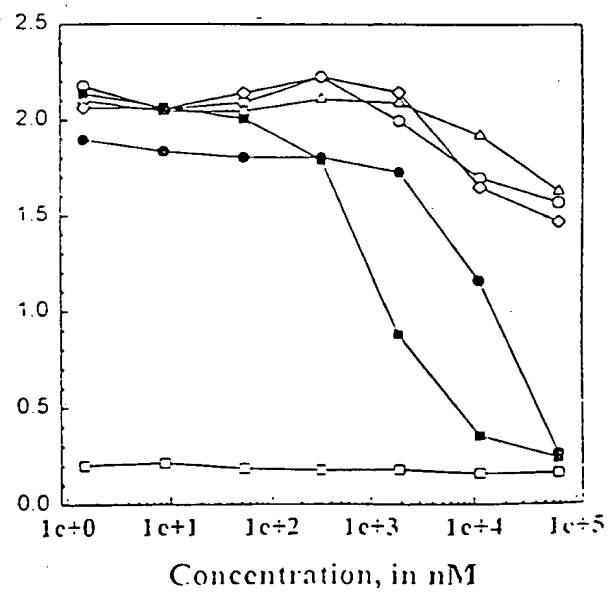


FIGURE 50D

FIGURE 51A

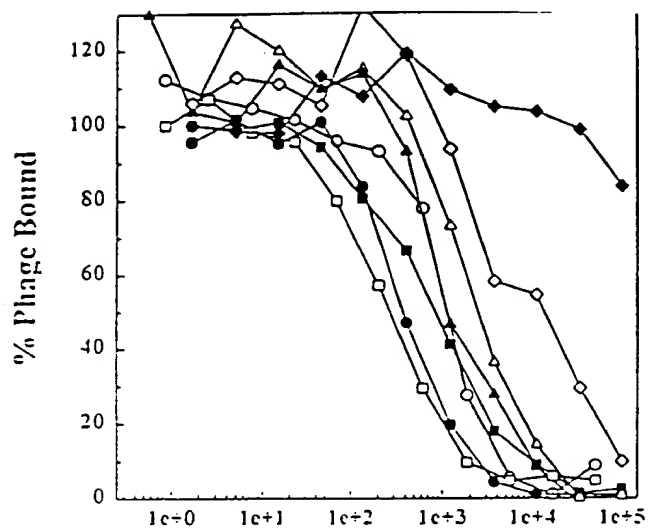


FIGURE 51B

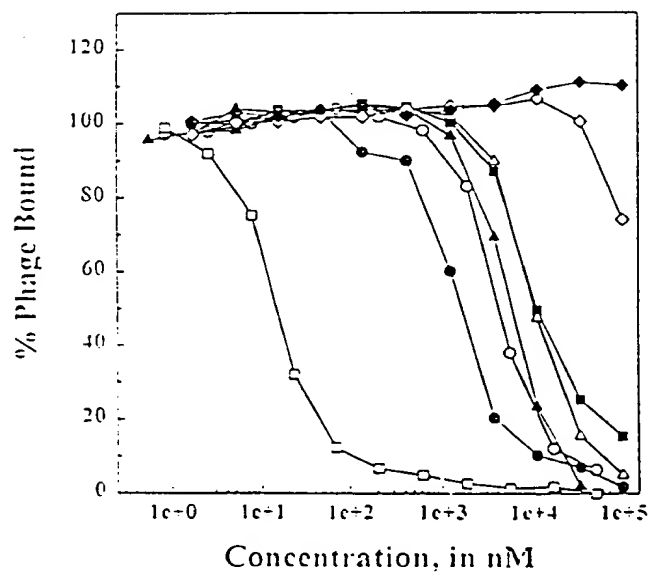
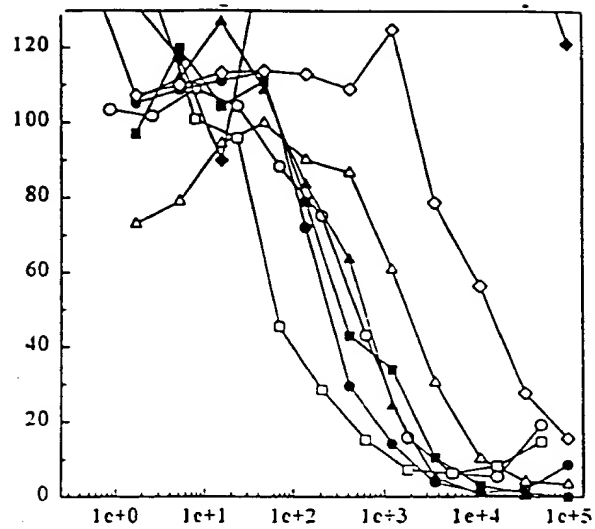


FIGURE 51C

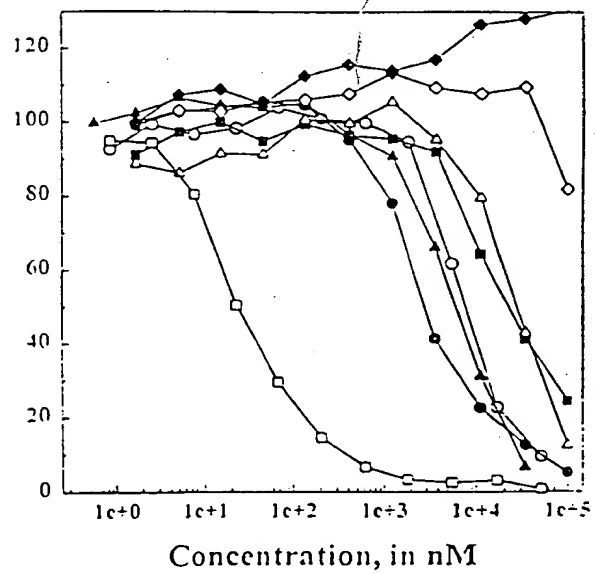


FIGURE 51D

FIGURE 52A

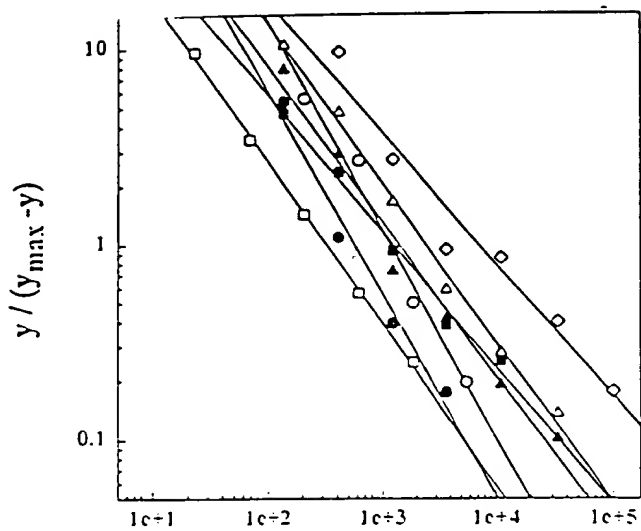


FIGURE 52B

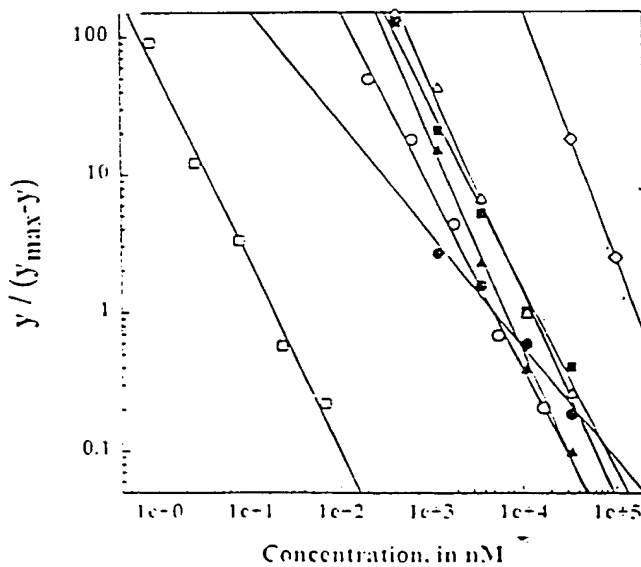
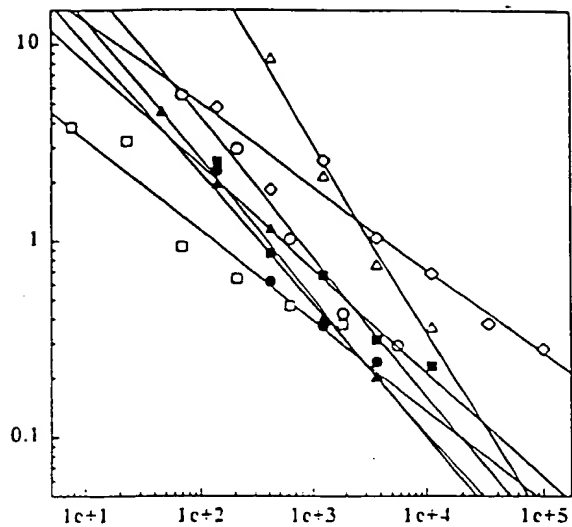


FIGURE 52C

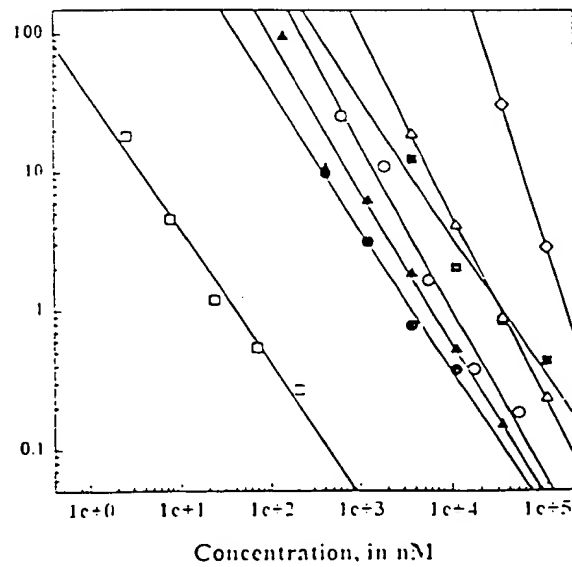


FIGURE 52D

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

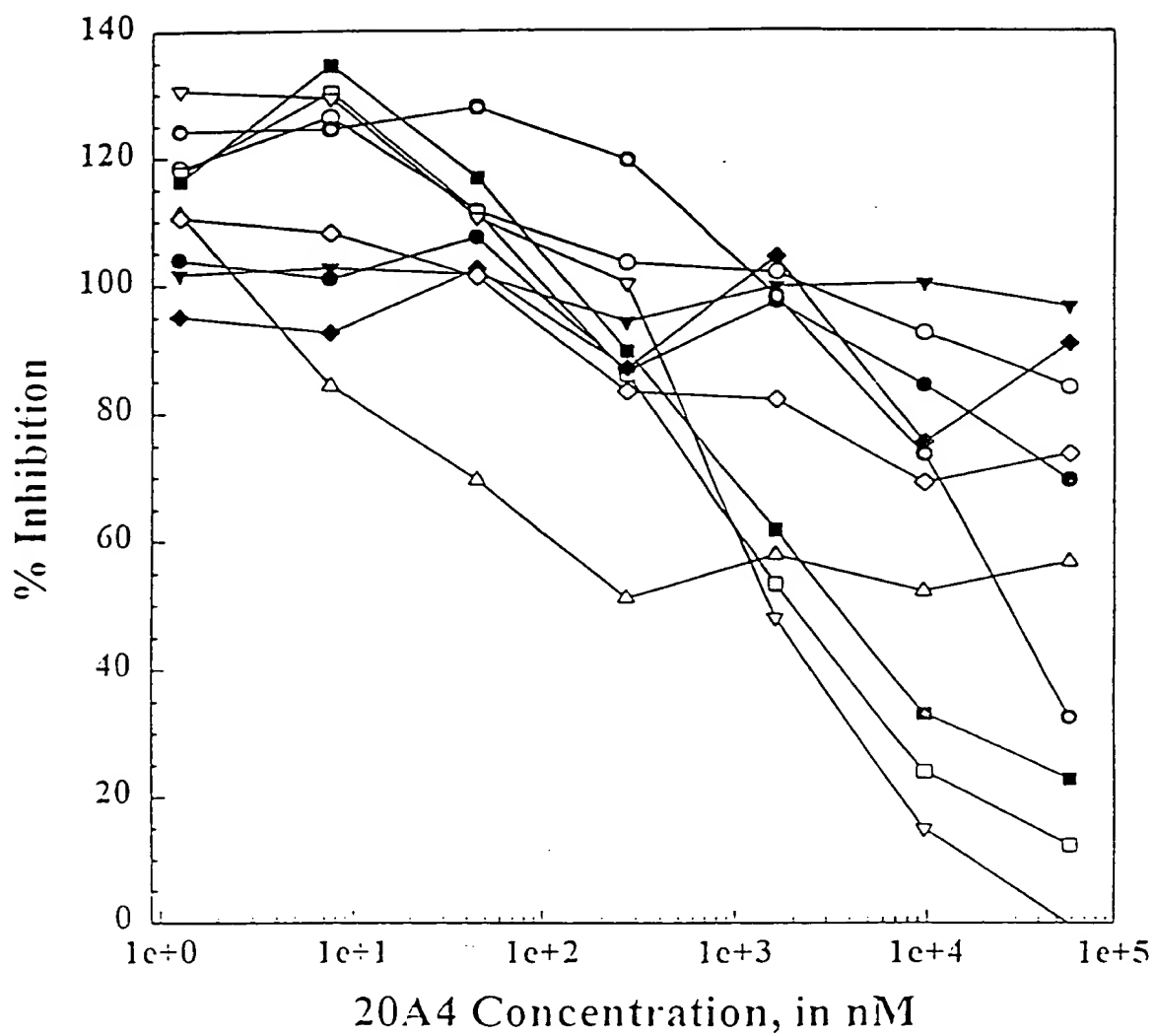


FIGURE 54

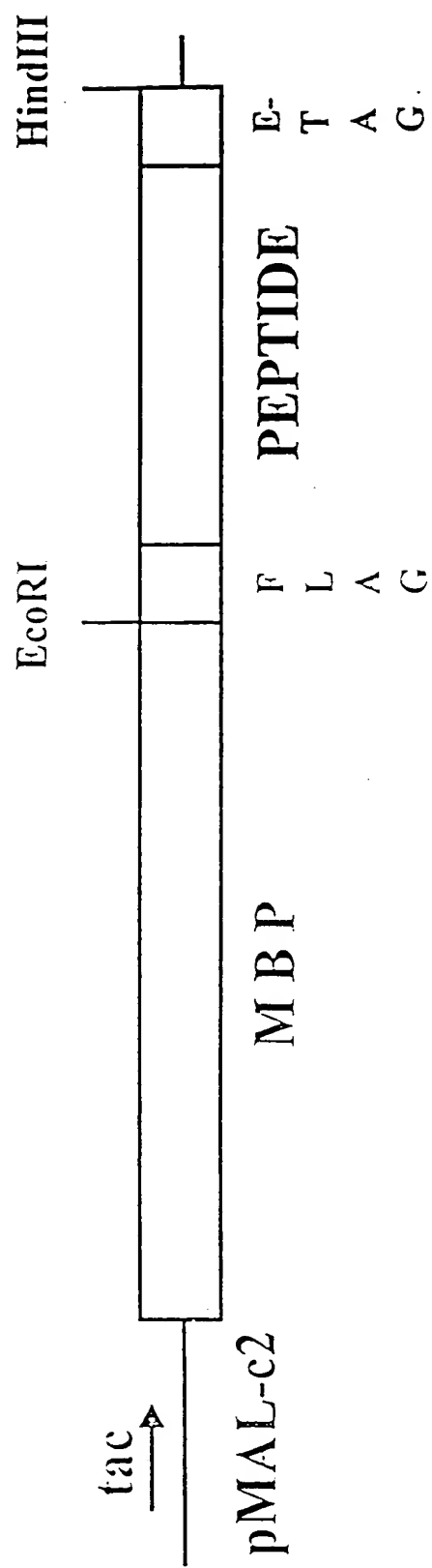


FIGURE 55

Normalized Phage Signal, % Control

FIGURE 56A

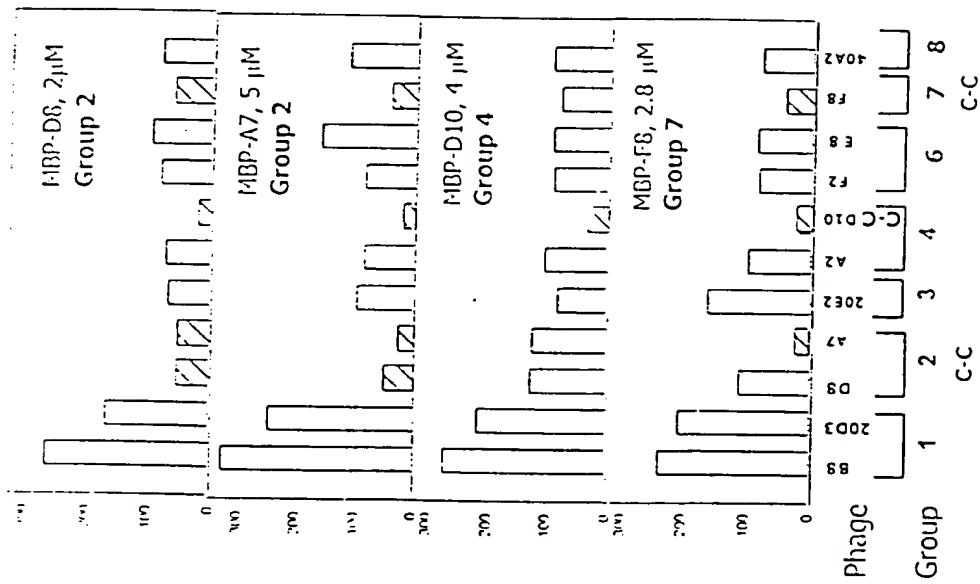


FIGURE 56B

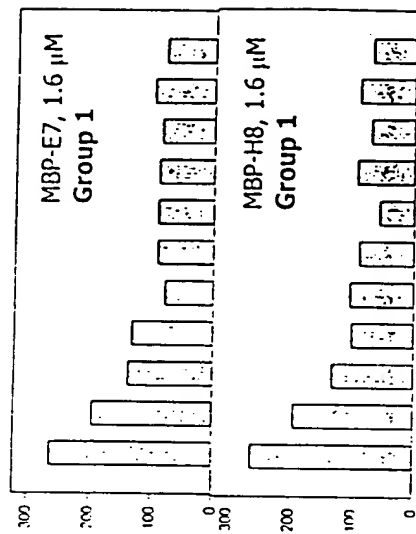
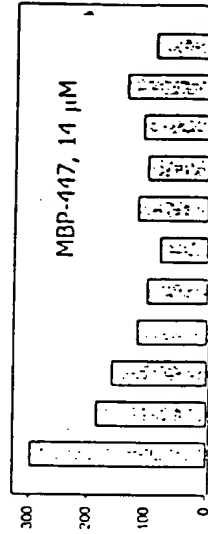


FIGURE 56C



10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCGA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCCT	GGTAAAGCCT	60
	E	V	Q	L	V	E
		S	G	G	L	V
						K
						P
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGOC	TCTGGATTCA	CTTTCAGTAA	CGCCTGGATG	120
G	G	S	L	R	L	S
		C	A	A	S	G
			F	T	F	S
					N	A
						W
						M
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAGCGAA	180
S	W	V	R	Q	A	P
		G	K	G	L	E
			W	V	G	R
					I	K
						S
						K
ACTGATGGTG	GGACAACAGA	CTACGCTGCA	CCCGTGAAG	GCAGATTCAC	CATCTCAAGA	240
T	D	G	G	T	T	D
		Y	A	A	P	V
			K	G	R	F
					T	I
						S
						R
GATGATTCAA	AAACACGGT	GTATCTGCA	ATGACAGOC	TGAAACCGA	GGACACAGOC	300
D	D	S	K	N	T	L
		Y	L	Q	M	N
			S	L	K	T
					E	D
						T
						A
GTGATTACT	GTACACATA	CGGCGACGTT	TACGACCGCG	ATTACGATGG	GCGTGGGGT	360
V	Y	Y	C	T	T	Y
		G	D	V	Y	D
			R	D	Y	D
					G	R
						W
						G
CAAGGACTC	TGGTCAOCT	CTCCTCAGT	GGAGGCGGTT	CAAGGAGG	TGGCTCTGGC	420
Q	G	T	L	V	T	V
		S	S	G	G	G
			S	G	G	G
					G	S
						G
						/
GGTGGGGT	CCGACATCA	GATGACCCG	TCTCATCTCT	CCCTGCTCTG	ATCTGTAGG	480
G	G	G	S	D	I	Q
		M	T	Q	S	P
			S	S	L	S
					A	S
						V
						G
GACGAGTCA	CCATCACTTG	CGGGGCGAGT	CAAGGACATTA	GCATTATTT	AGCCTGGTAT	540
D	R	V	T	I	T	C
		R	A	S	Q	G
			I	S	N	Y
					L	A
						W
						Y
CAAGGAAAC	CAAGGAAAT	TCTTAGGTC	CTGATCTATG	CTGCTCCAC	TTTGGATCA	600
Q	Q	K	P	G	K	V
		P	K	L	L	I
			Y	A	A	S
					T	L
						Q
						S
GGGTCCCT	CTGGTTCAG	TGGTGTGGA	TCTGGGACG	ATTTCCTCT	CACTTCAGT	660
G	V	P	S	R	F	S
		G	S	G	S	G
			T	D	F	T
					L	T
						I
						S
AGCCTGAGC	CTGAGATGT	TGCACTTAT	TACTGTGCA	ASTATAACG	TGCCCCCTTC	720
S	L	Q	P	E	D	V
		A	T	Y	Y	C
			Q	K	Y	N
					S	A
						P
						F
ACTTTCGAC	CTGGAACAA	AGTGTATTC	AAACGGGCG	C		761
T	F	G	P	G	T	K
		V	D	I	K	

FIGURE 57

CLONES		VHCDR3			
%Inhibition Activity					
	118:	PFFV	FY <u>RG</u> QDT	54%	
?	InsulB:	FVNQH <u>L</u> <u>CGSH</u> <u>L</u> <u>VE</u> <u>ALY</u>	<u>L</u> <u>V</u> <u>CG</u> <u>ER</u> <u>G</u> <u>F</u> <u>Y</u> <u>T</u> <u>P</u> <u>K</u> <u>T</u>		
	12H10:	C	VVYNYA	G RG T	42%
Ang?	13-e-4:		VQAWDGL	G RES	52%
?	13h9:		GGL	G RRDWL	30%
?	24:		GGRR	H RLG	
	InsulinA	GIVEQCQCTSI <u>C</u> SLYQ	<u>LE</u> NYCN		
	11a8:		ENYGNSE		32%
?			GDQELQNY		None
	N/A				

FIGURE 59

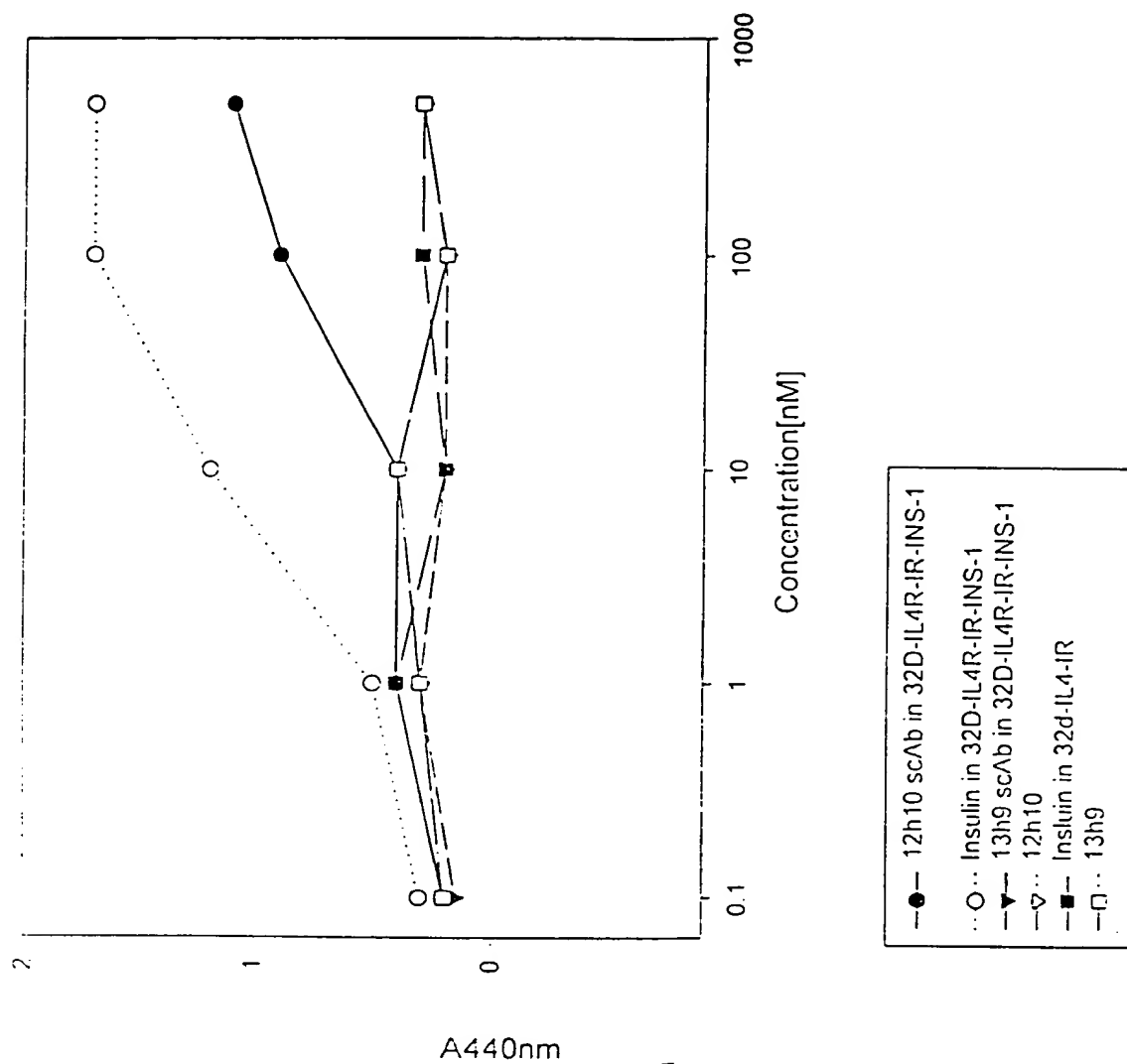


FIGURE 60

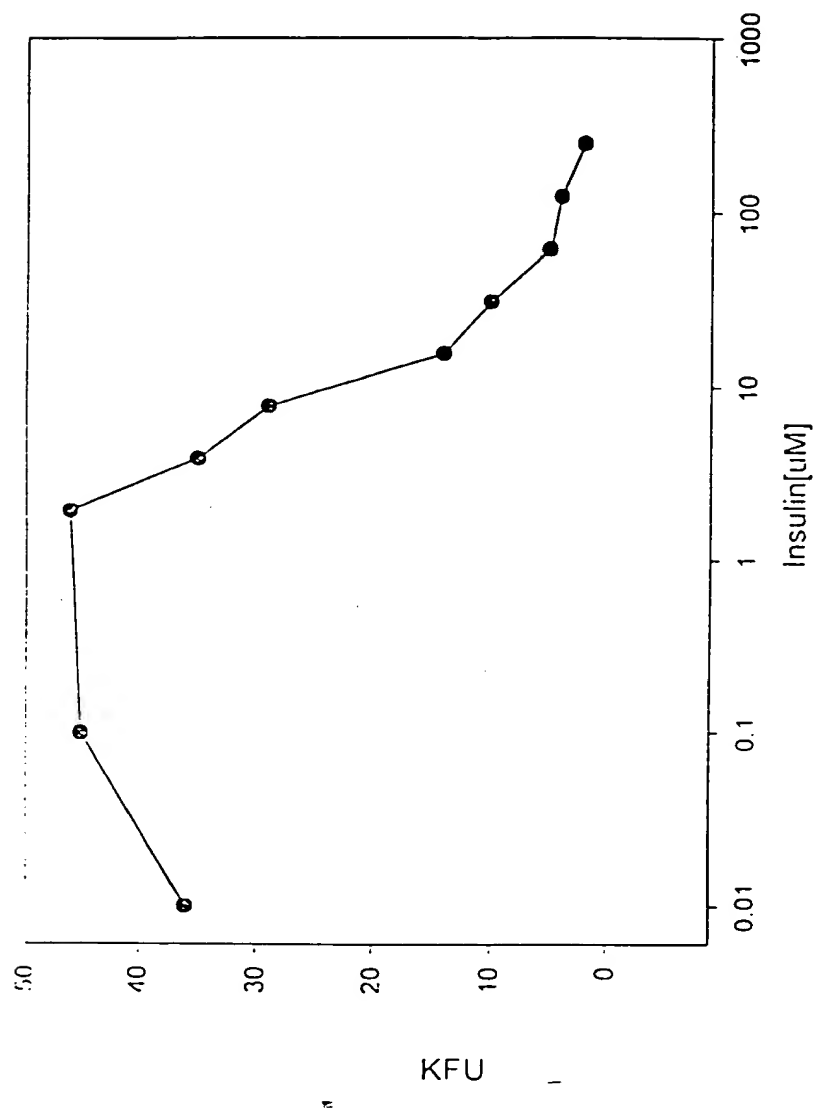


FIGURE 61



Concentration (nM)	C1	G1-2DD1	G2-D8	G3-2DC11	H2	2DA4	2A9
0.001	0	0	0	0	0	0	0
0.01	0	0	0	0	0	0	0
0.1	0	0	0	0	0	0	0
1	100	150	200	250	100	50	150
10	400	600	800	1400	300	150	1000
100	1100	1300	1950	2050	400	400	900



00620" 00000000

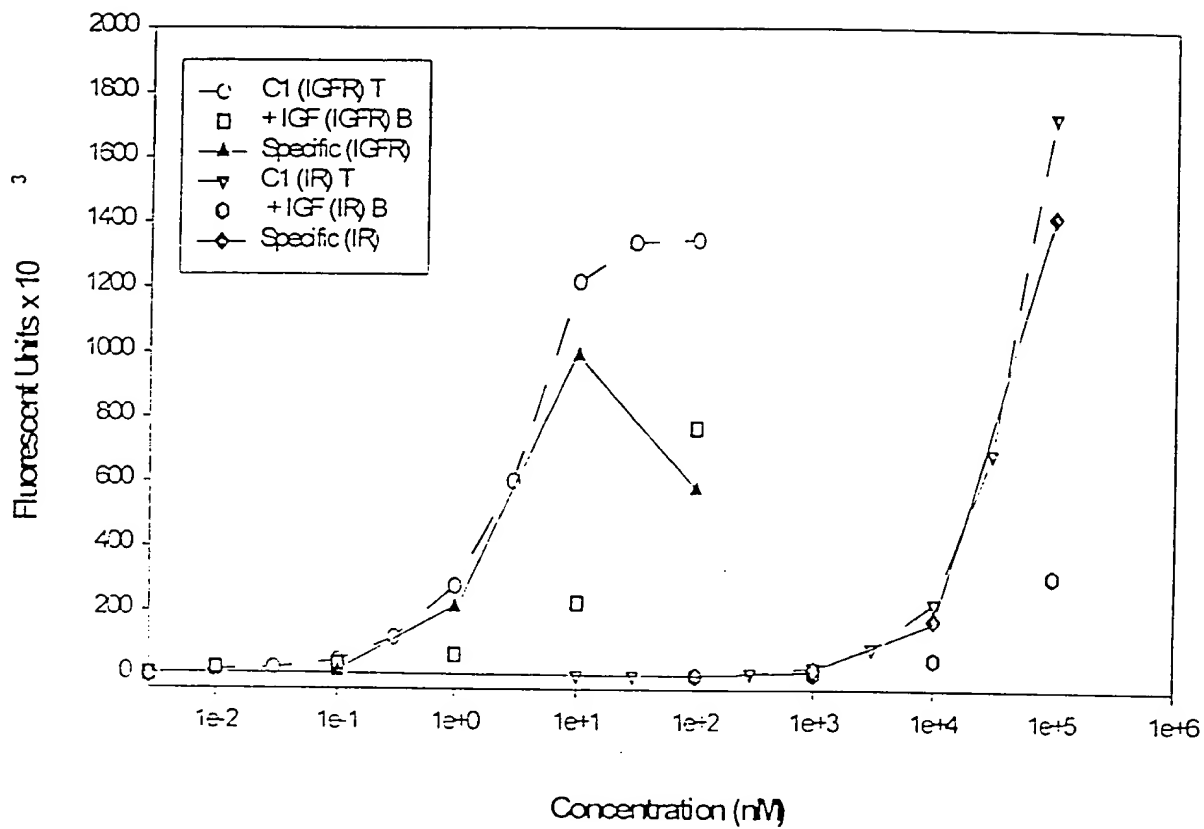


FIGURE 64

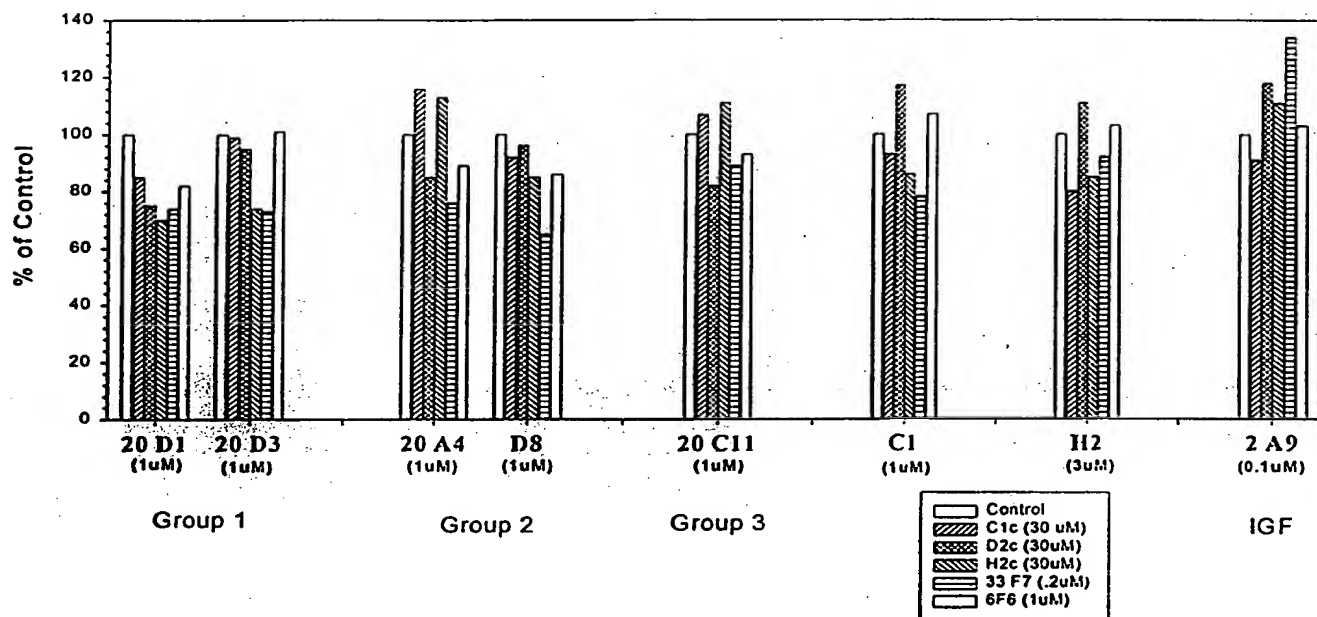


FIGURE 65

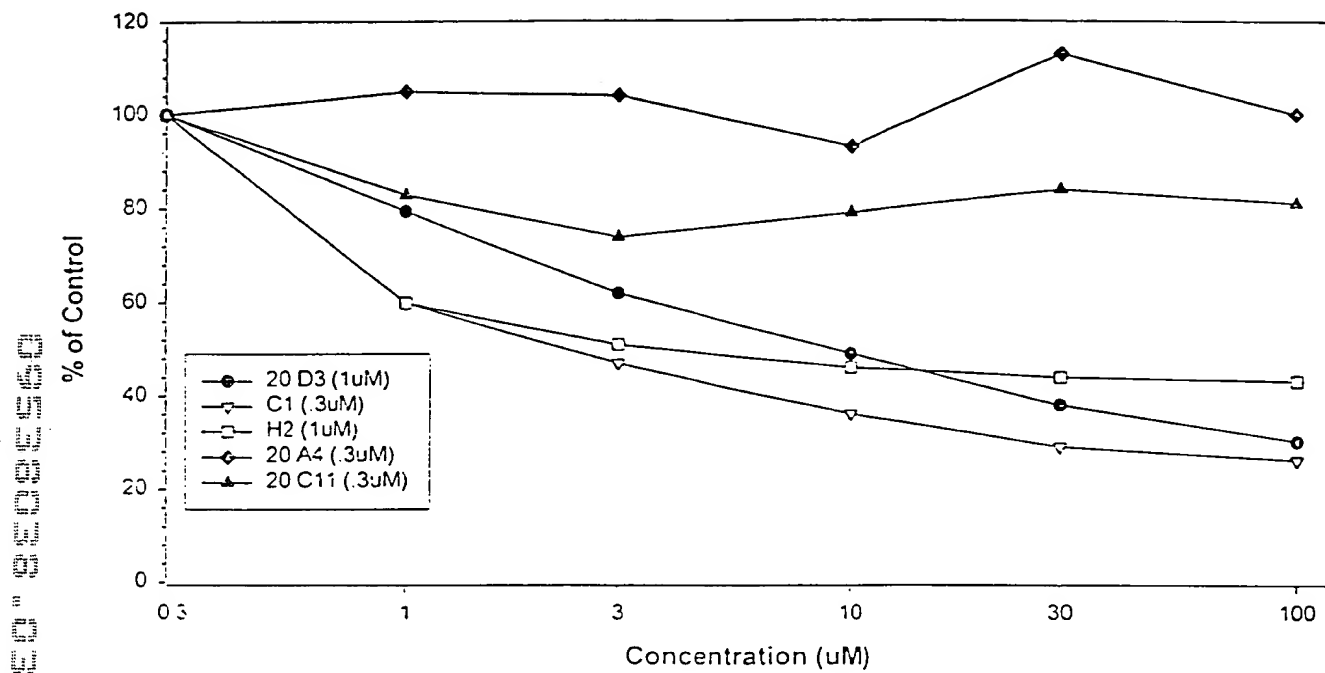


FIGURE 66

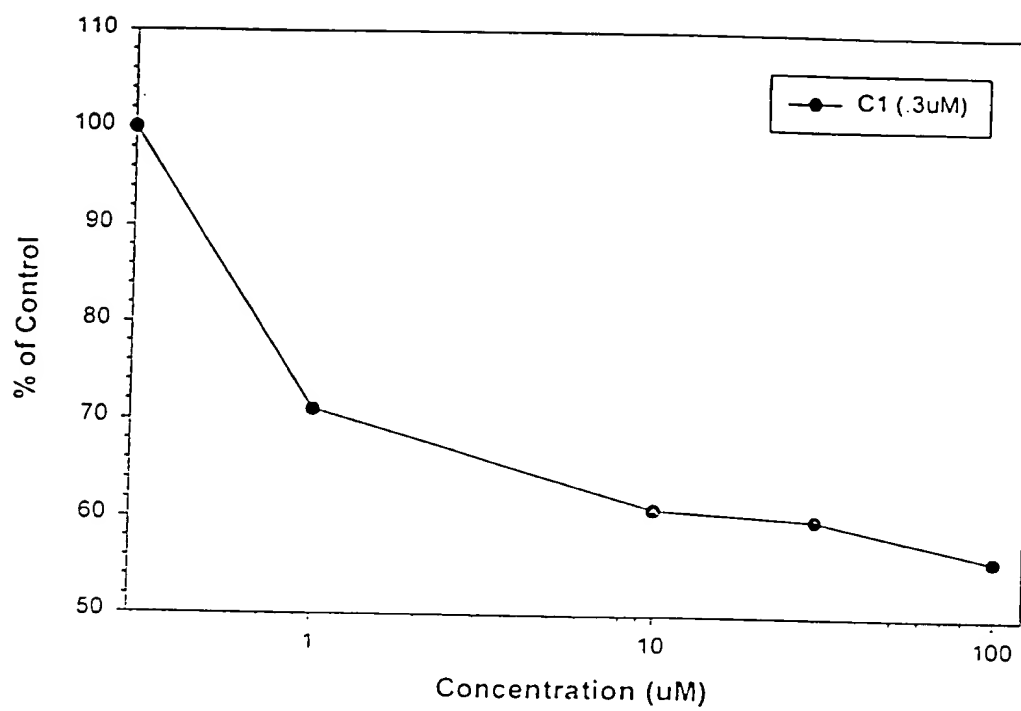


FIGURE 67

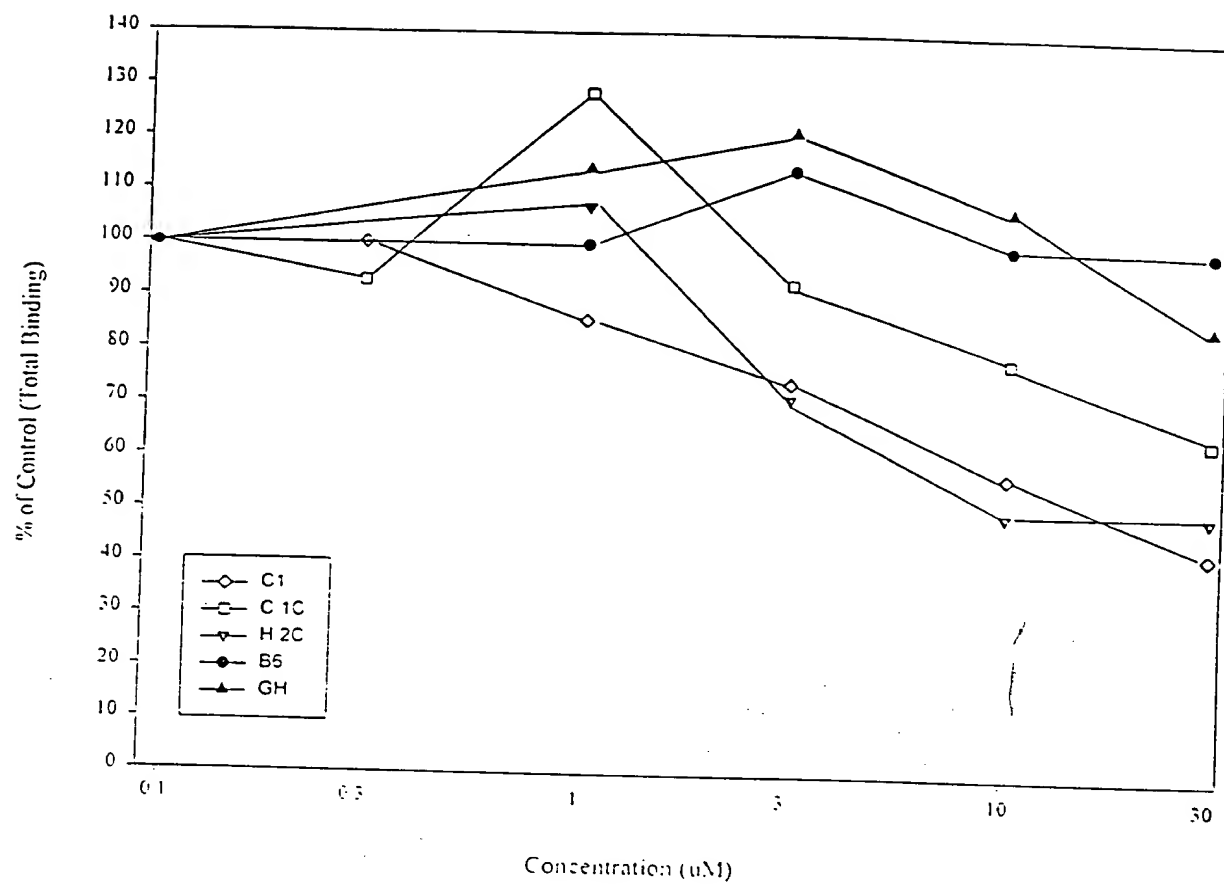


FIGURE 68

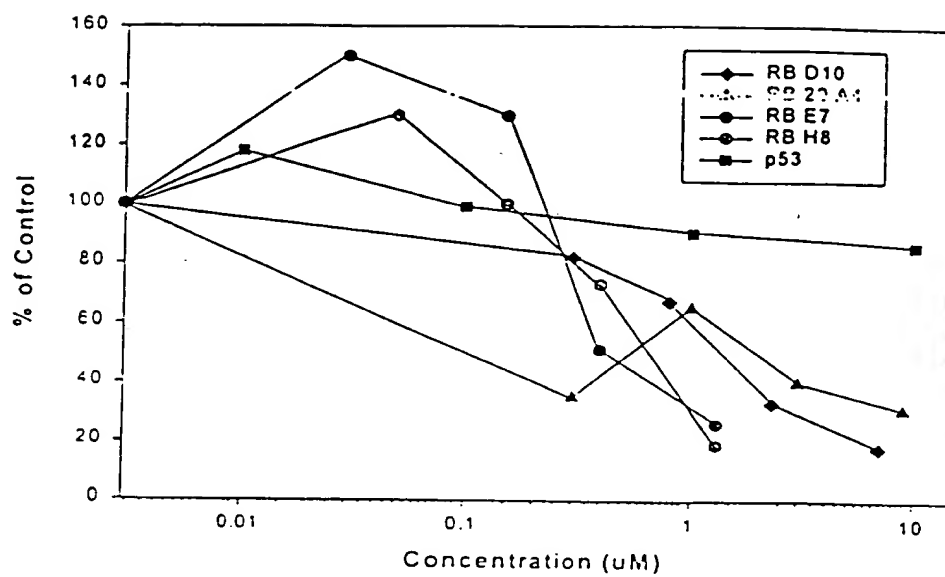


FIGURE 69

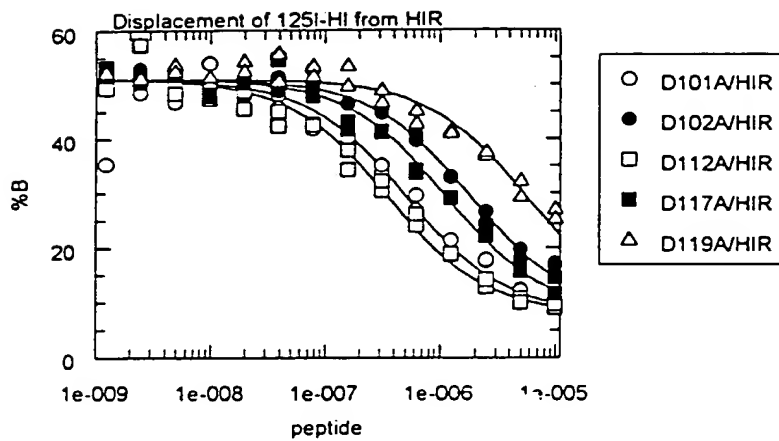


FIGURE 70A

D990114A

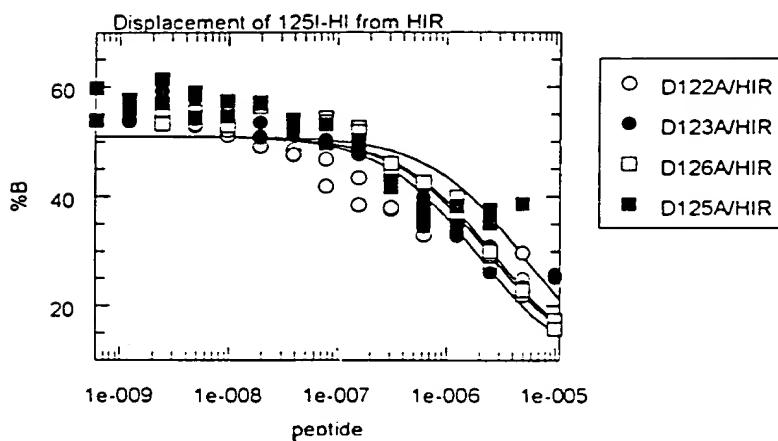


FIGURE 70B

D990118A

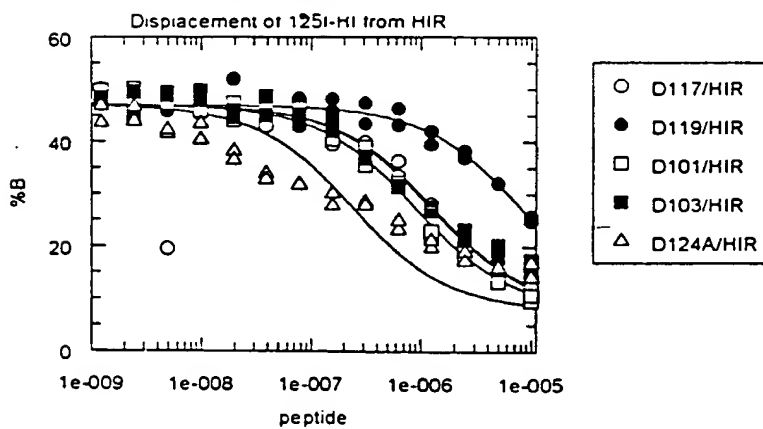


FIGURE 70C

D990126A

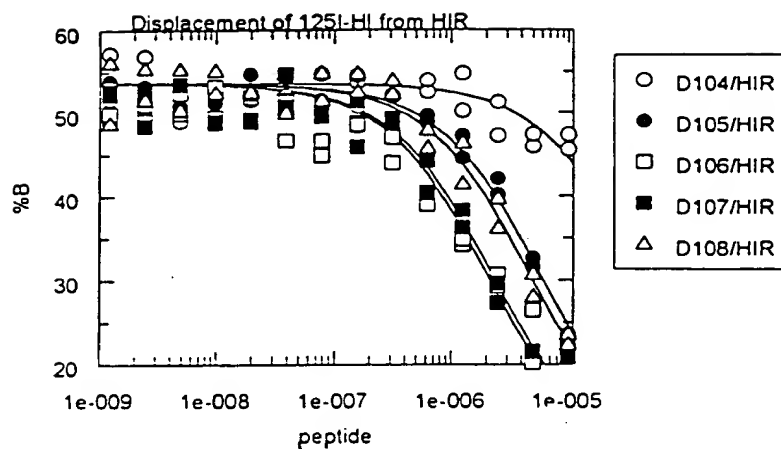


FIGURE 70D

D990129A

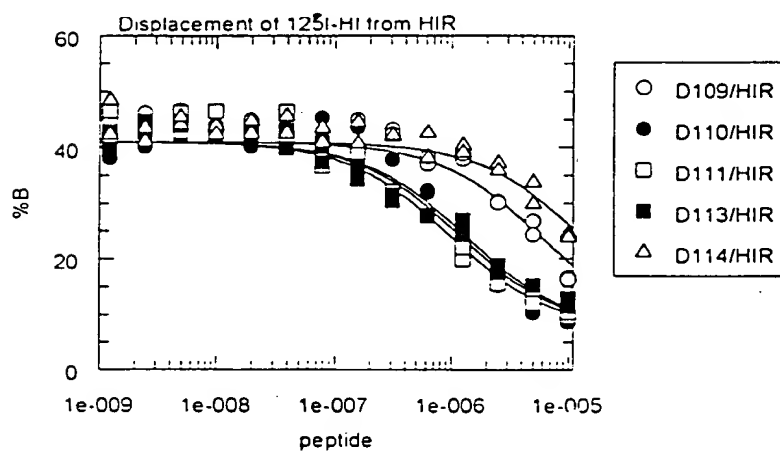


FIGURE 70E

D990202A

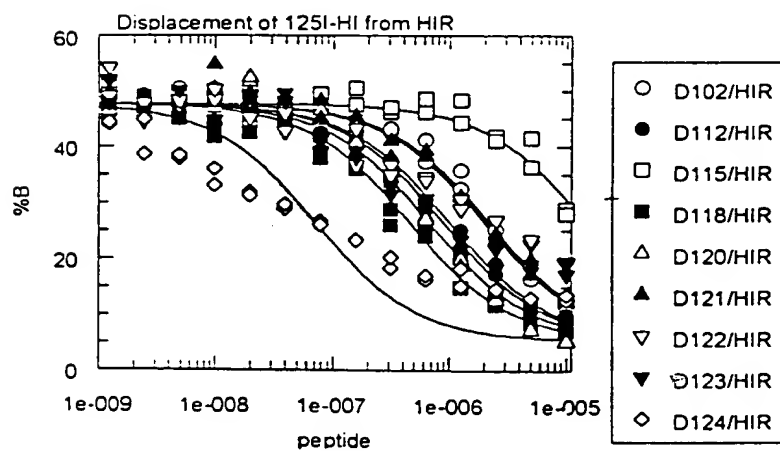


FIGURE 70F

D990205A

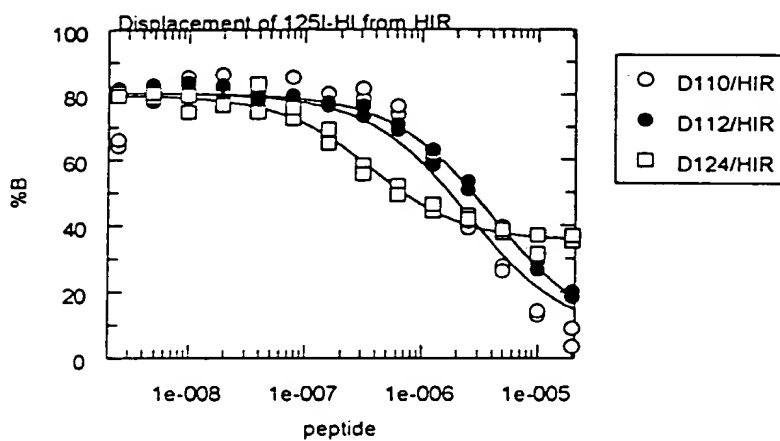


FIGURE 70G

D990217A

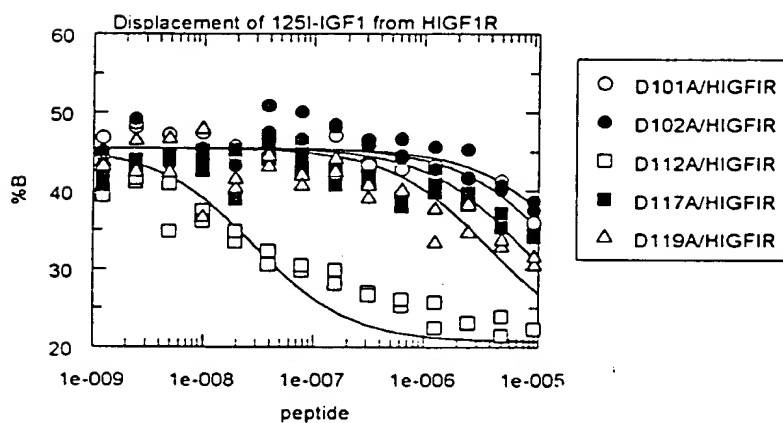


FIGURE 70H

D990114A

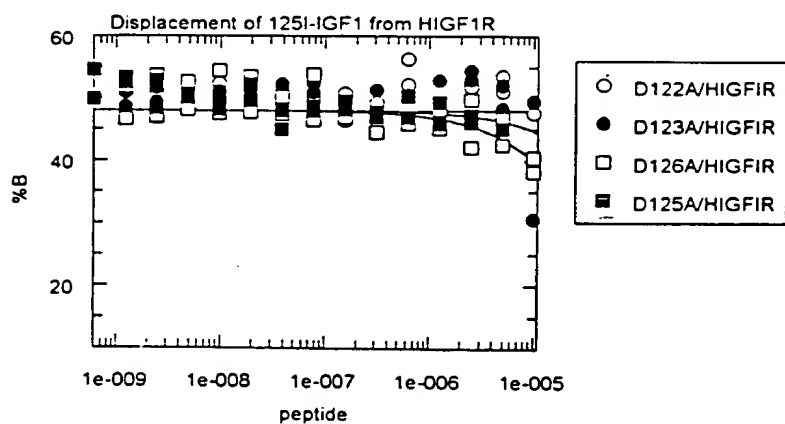


FIGURE 70I

D990118A

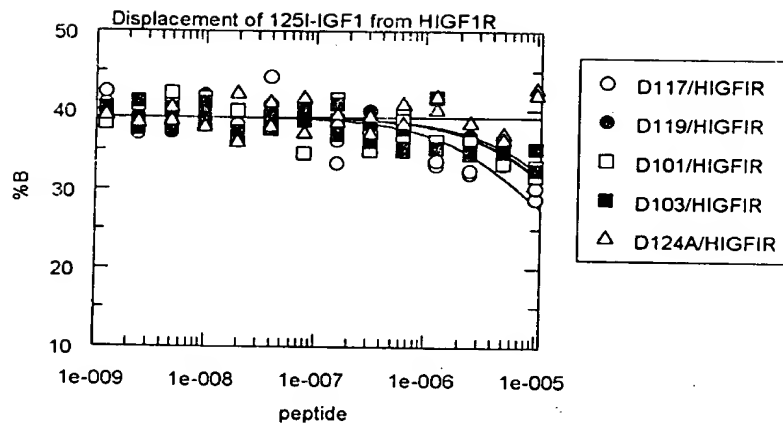


FIGURE 70J

D990126A

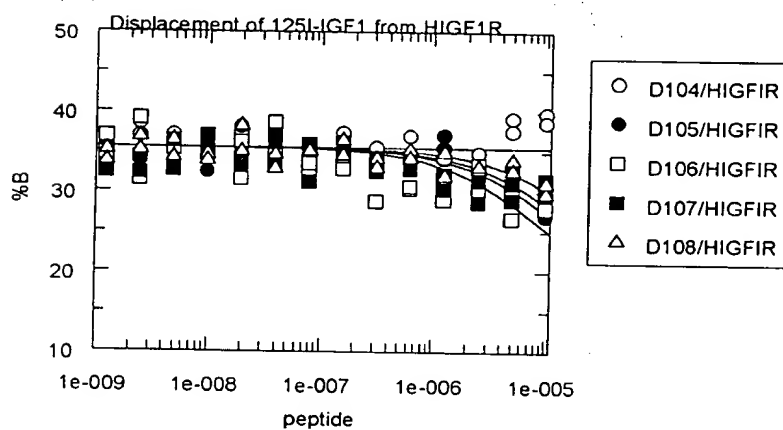


FIGURE 70K

D990129A

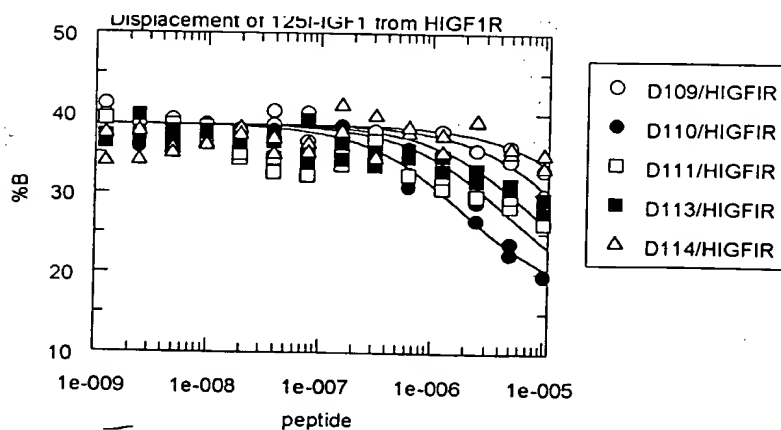


FIGURE 70L

D990202A

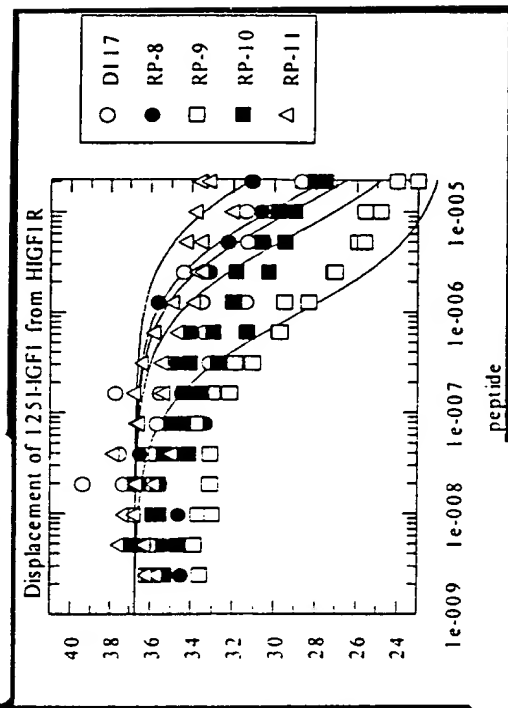
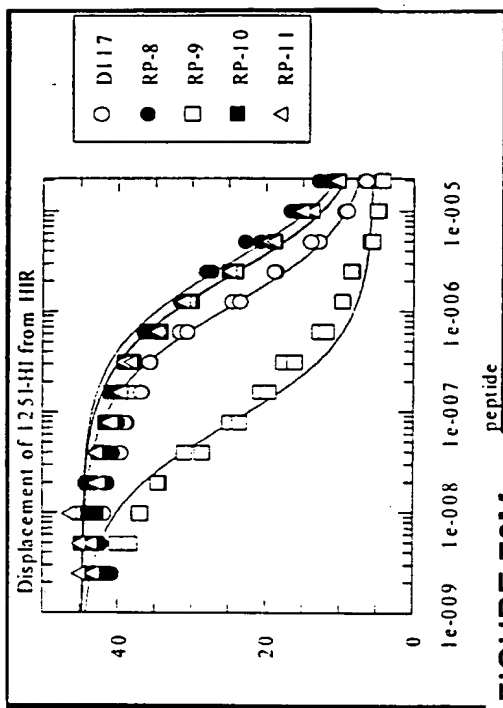


FIGURE 71A

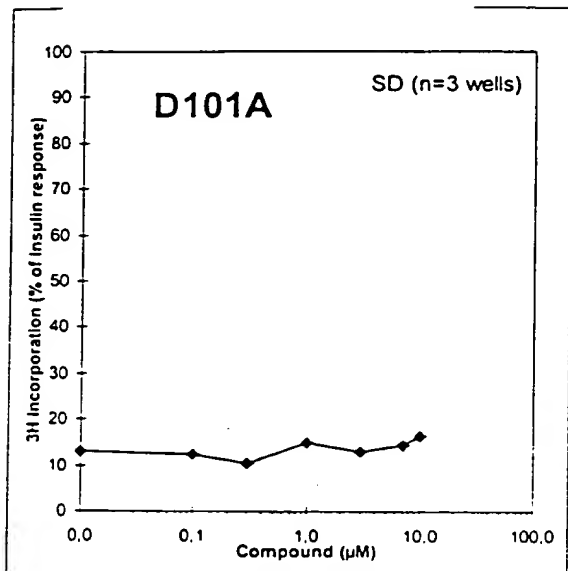


FIGURE 71B

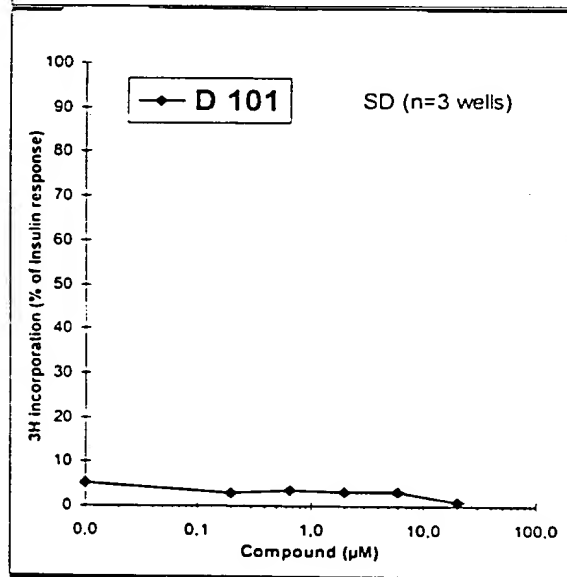
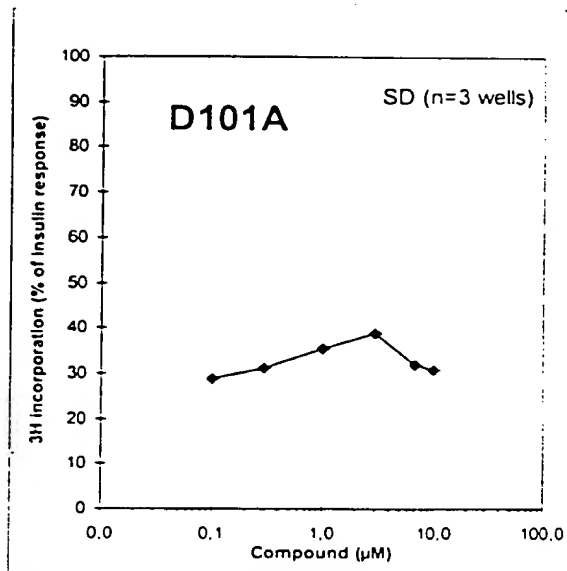


FIGURE 71C

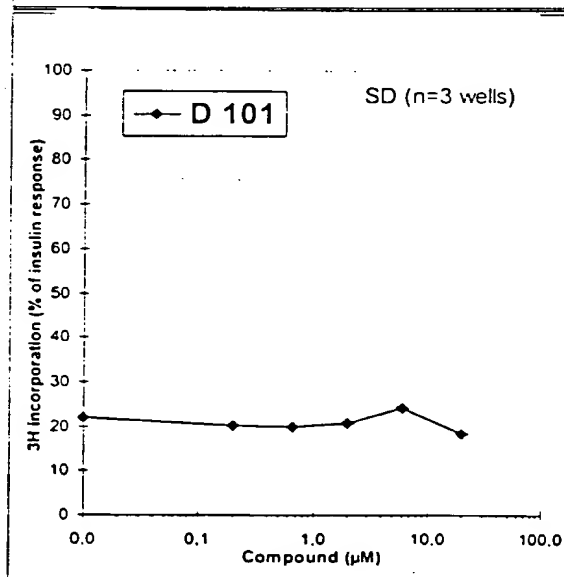


FIGURE 71D

FIGURE 71E

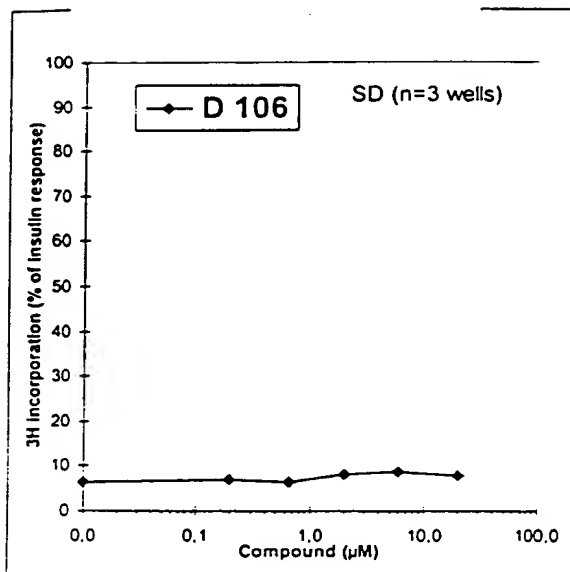


FIGURE 71F

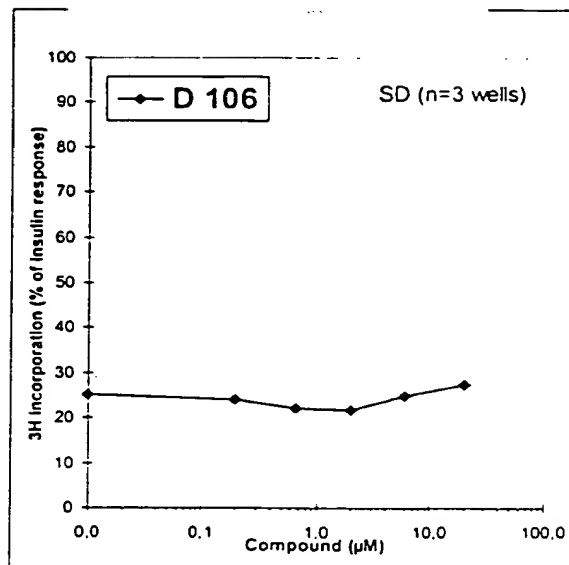


FIGURE 71G

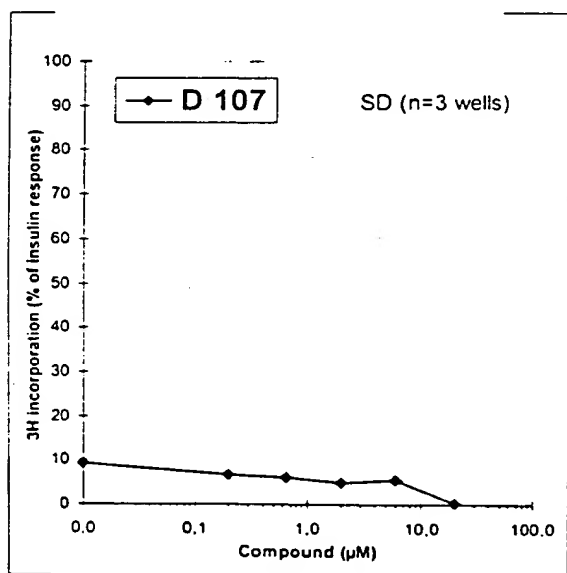


FIGURE 71H

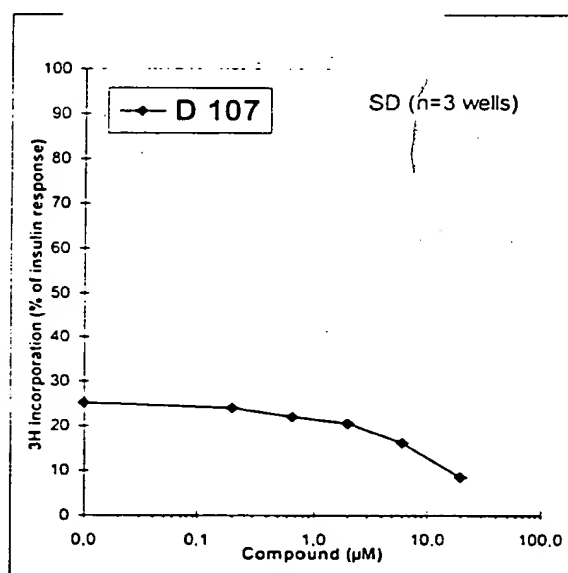


FIGURE 71I

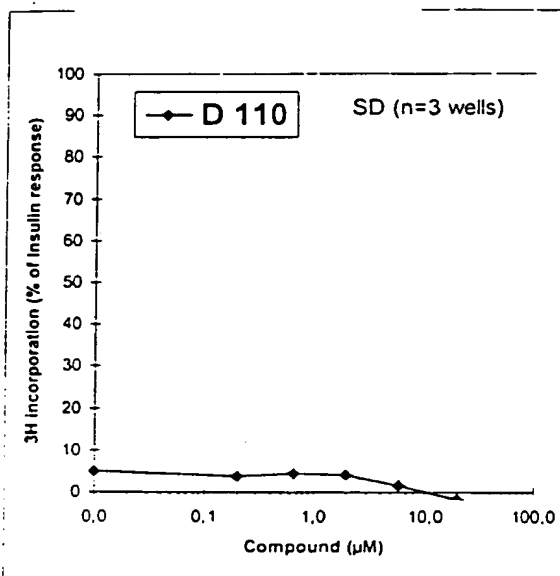


FIGURE 71J

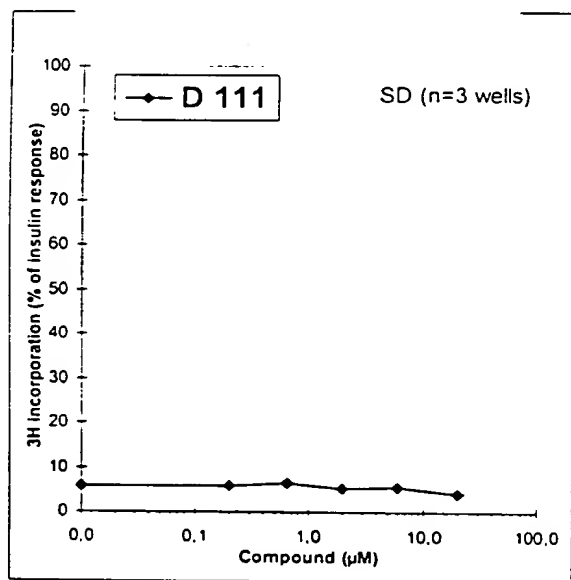
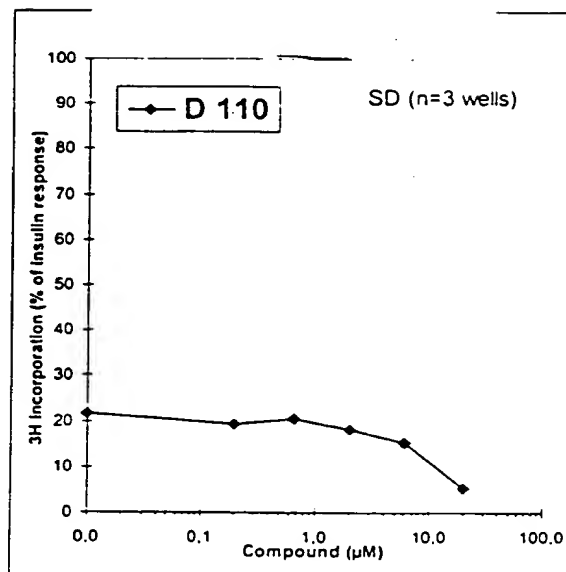


FIGURE 71K

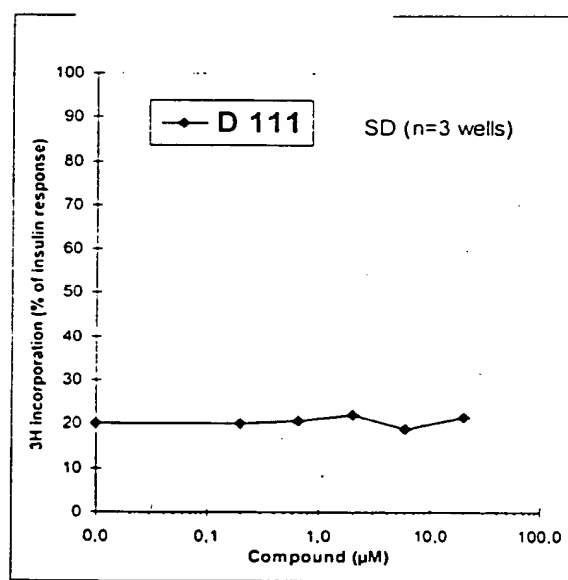


FIGURE 71L

FIGURE 71M

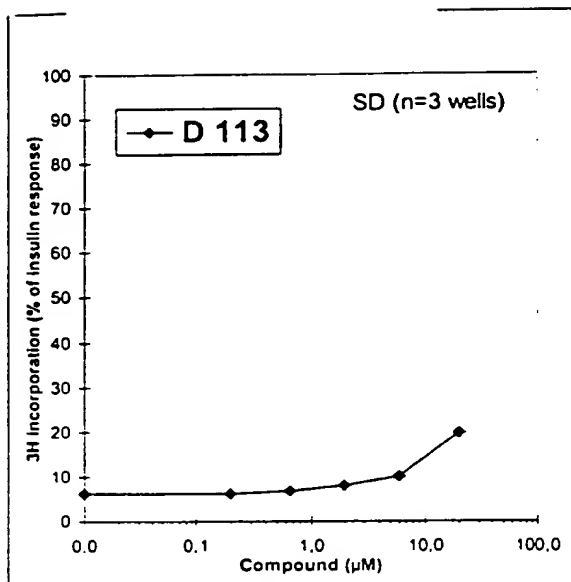


FIGURE 71N

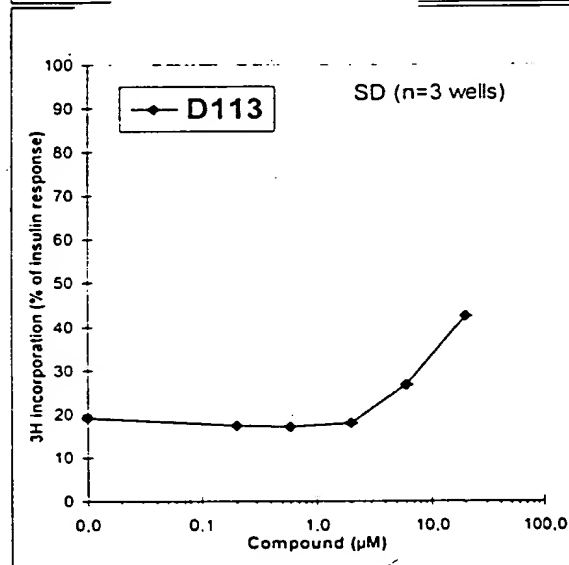
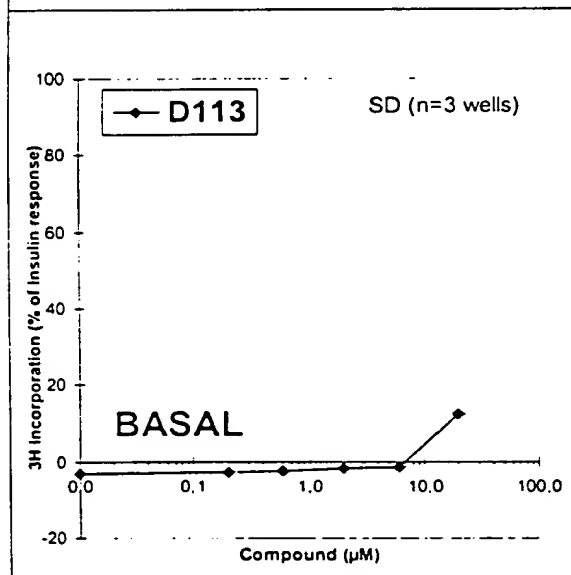
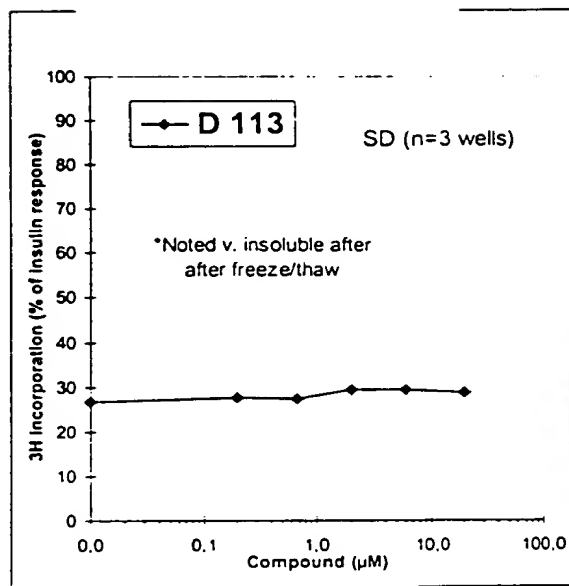


FIGURE 71O

FIGURE 71P

FIGURE 71Q

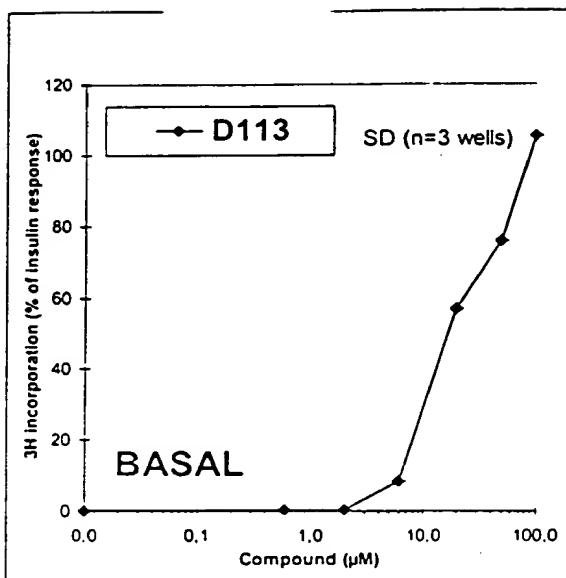


FIGURE 71R

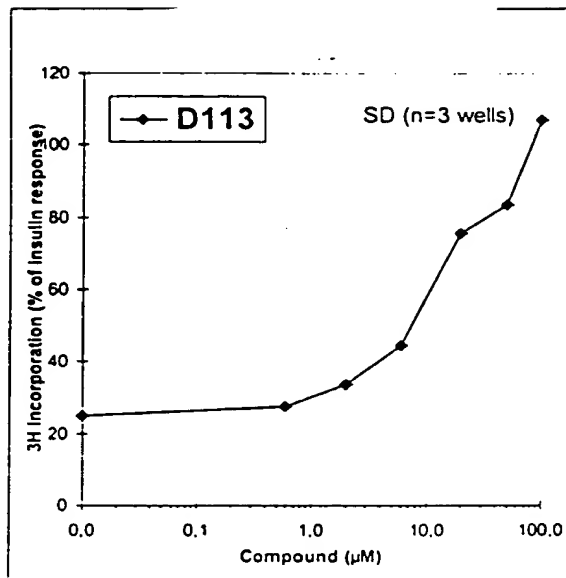


FIGURE 71S

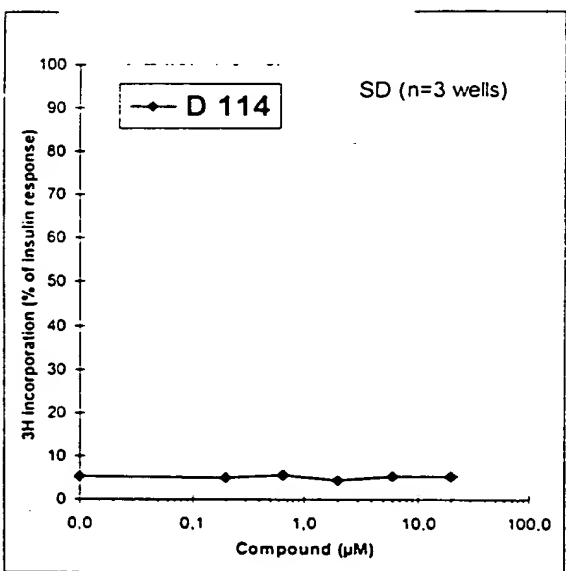


FIGURE 71T

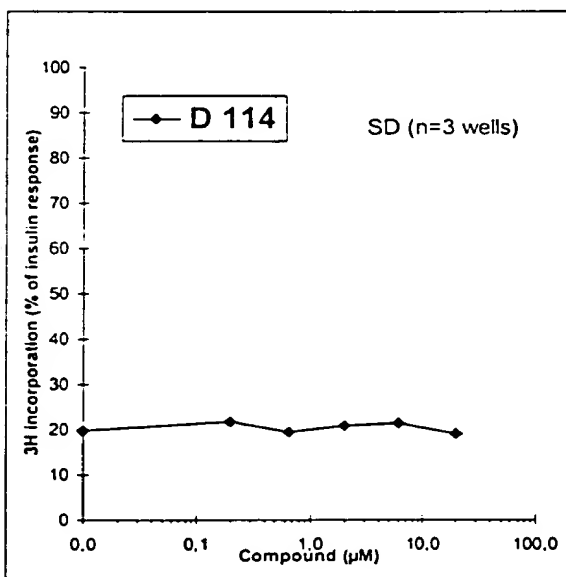


FIGURE 71U

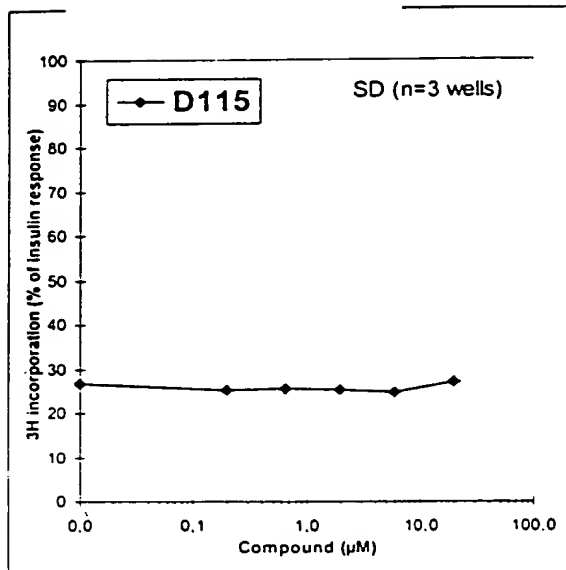


FIGURE 71V

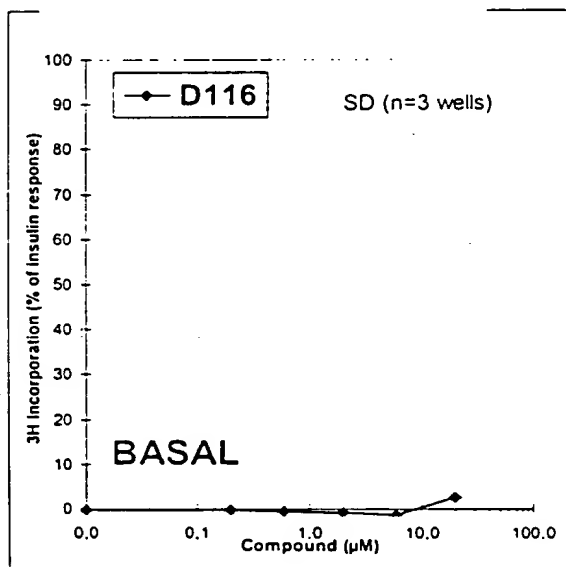
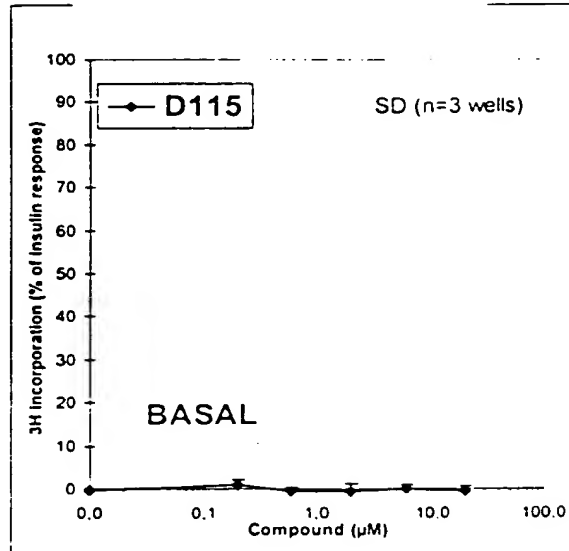


FIGURE 71W

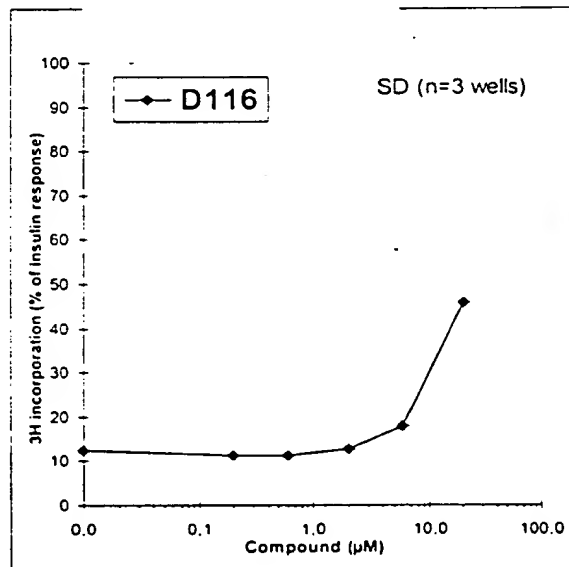


FIGURE 71X

FIGURE 71Y

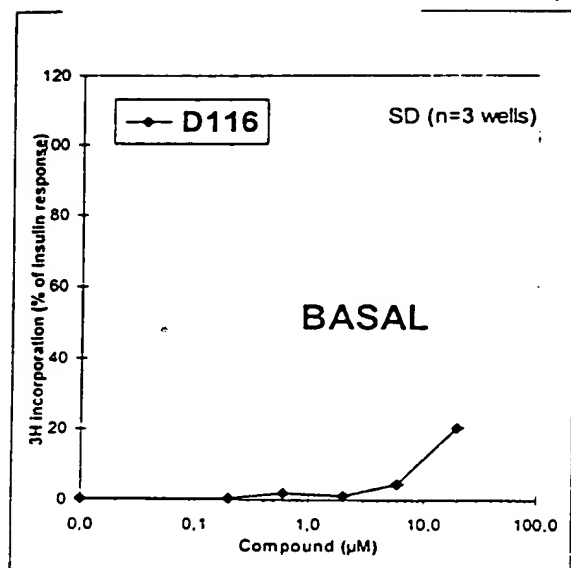


FIGURE 71Z

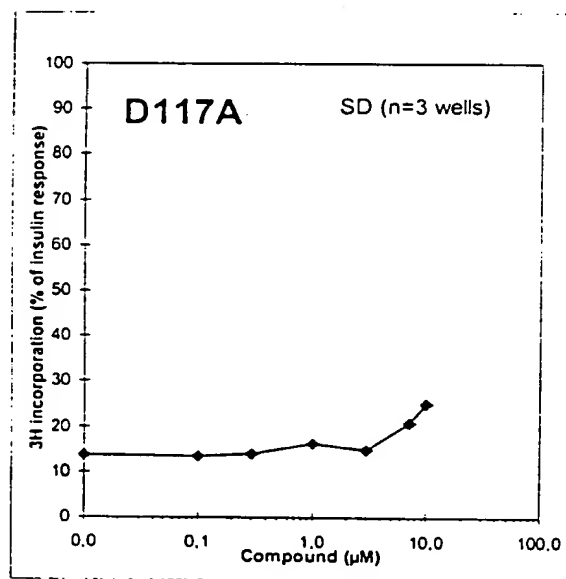
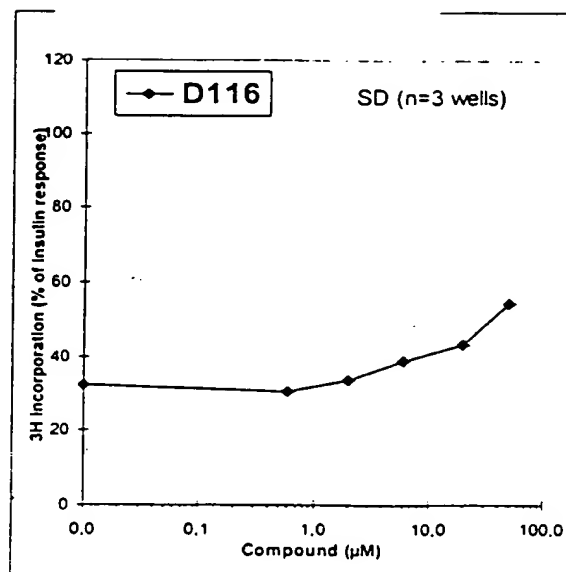


FIGURE 71A2

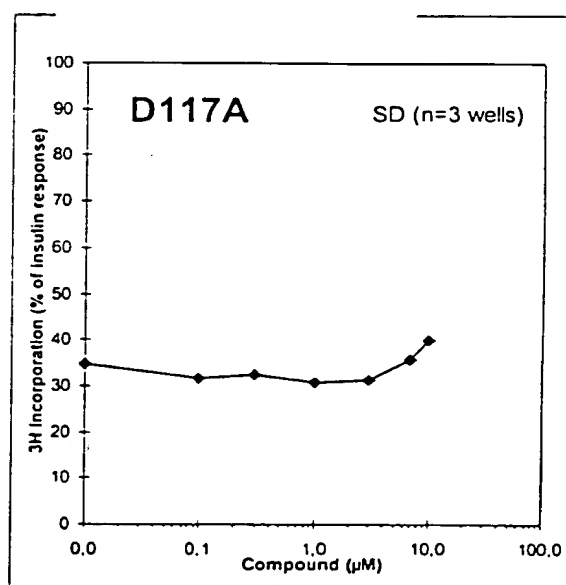


FIGURE 71B2

FIGURE 71C2

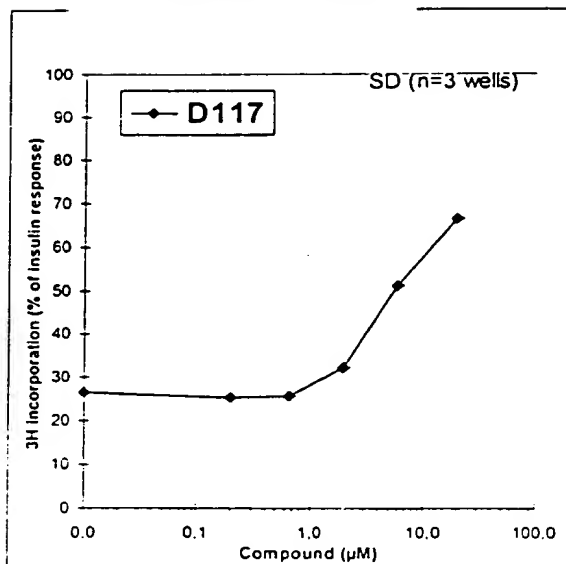


FIGURE 71D2

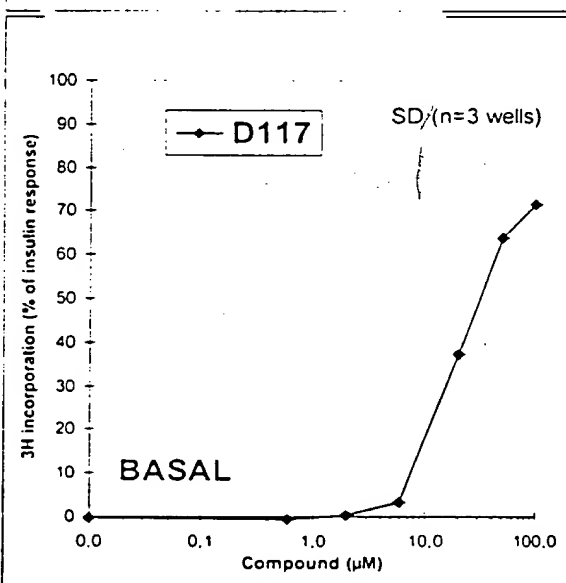
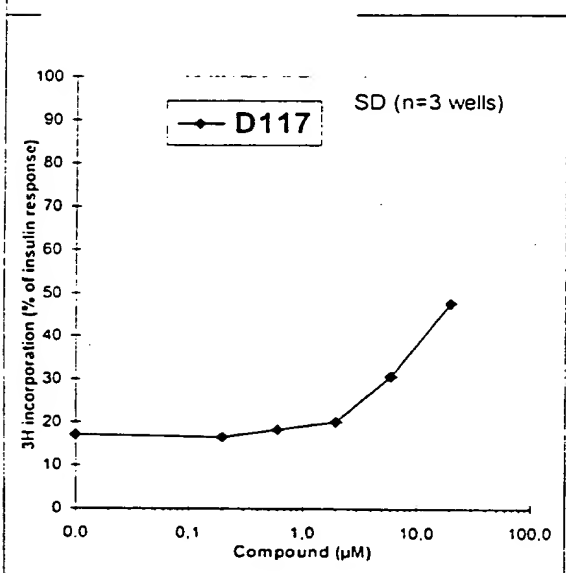
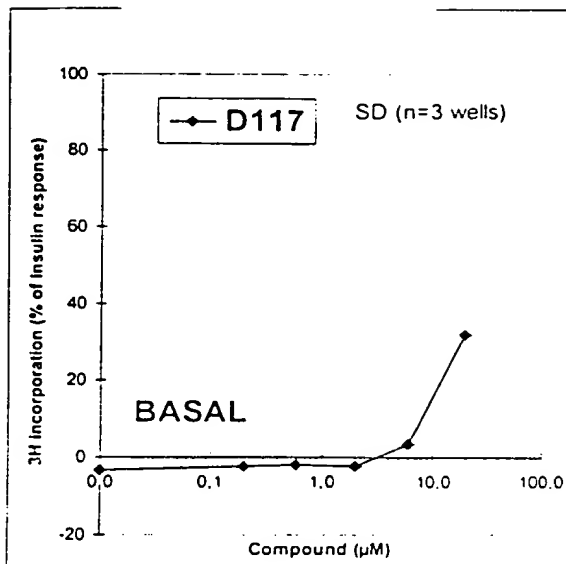


FIGURE 71E2

FIGURE 71F2

FIGURE 71G2

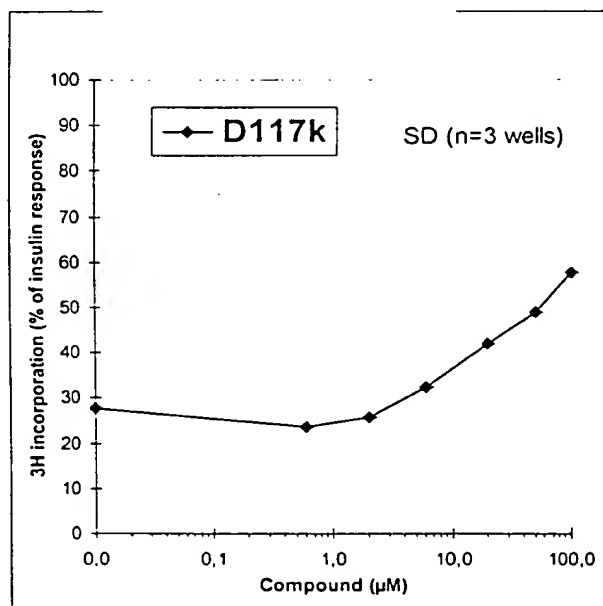
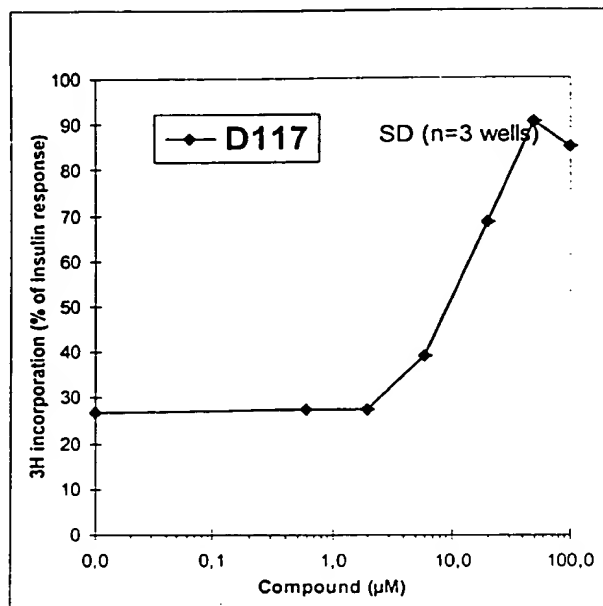


FIGURE 71H2

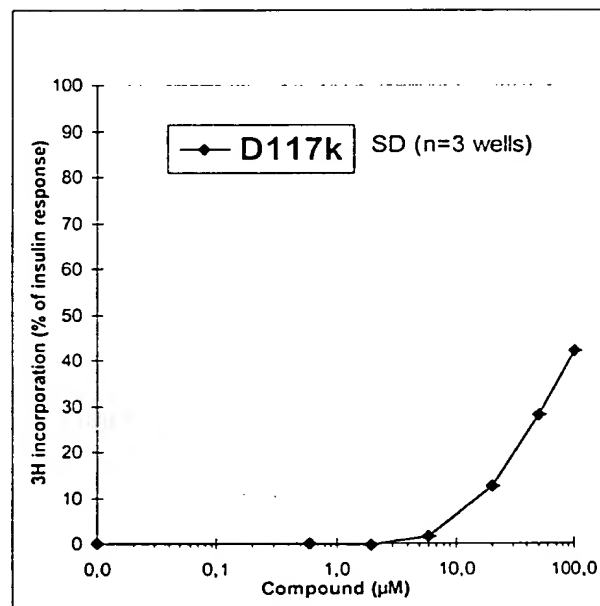


FIGURE 71I2

FIGURE 71J2

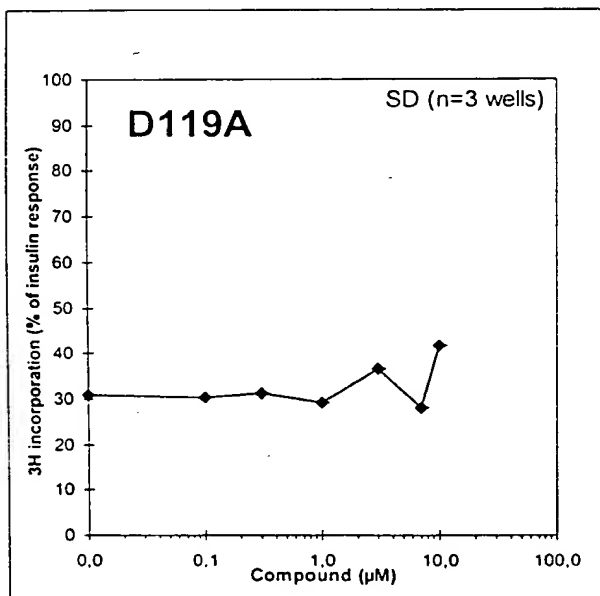
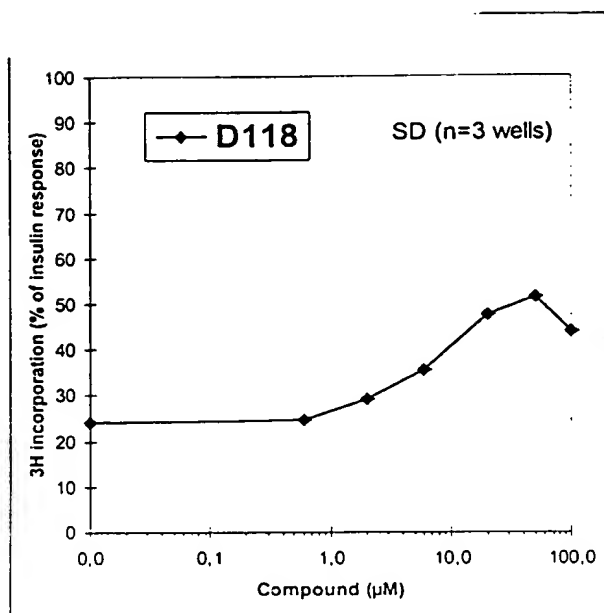


FIGURE 71K2

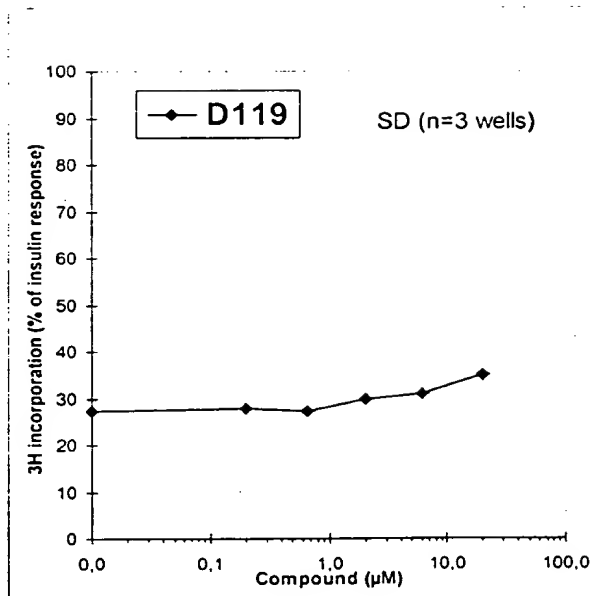


FIGURE 71L2

FIGURE 71M2

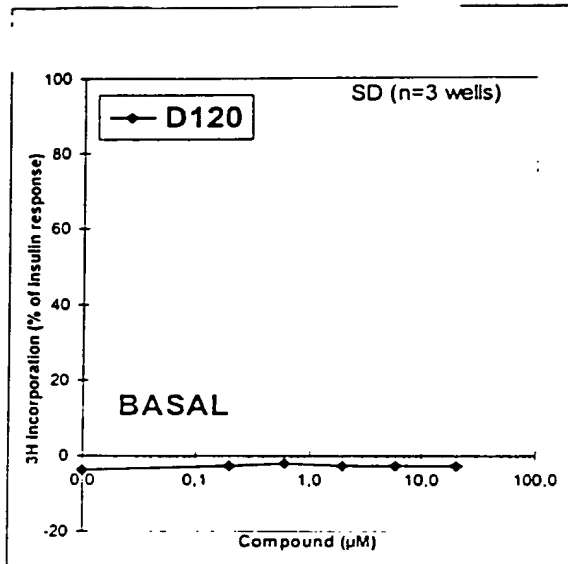


FIGURE 71N2

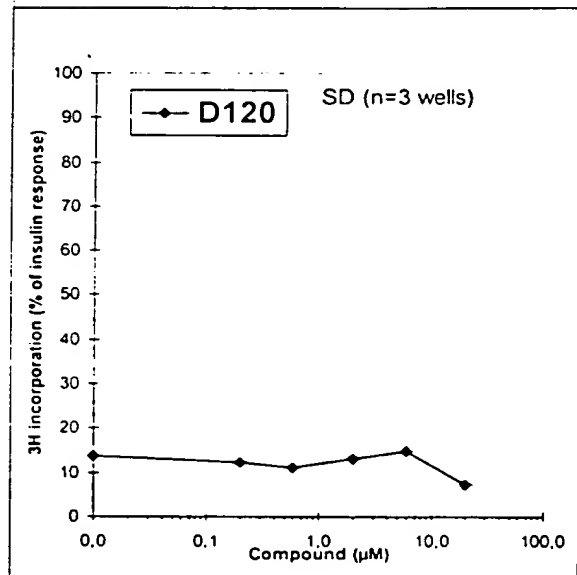
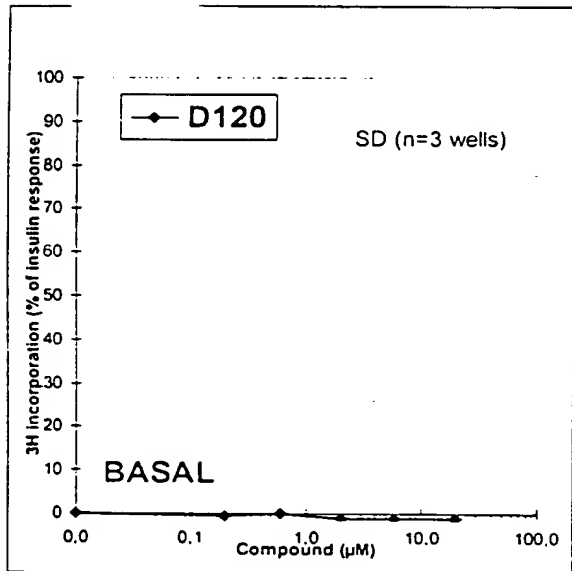
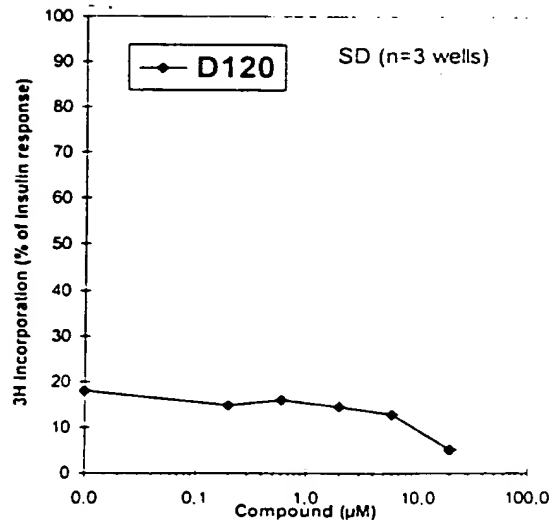


FIGURE 71O2

FIGURE 71P2

FIGURE 71Q2

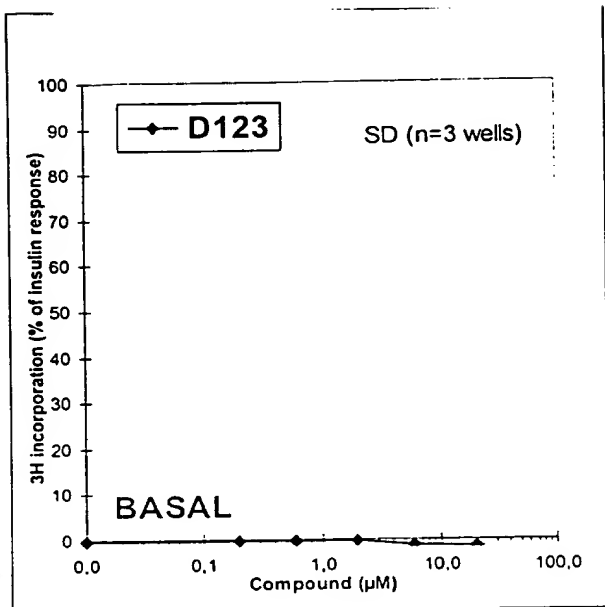


FIGURE 71R2

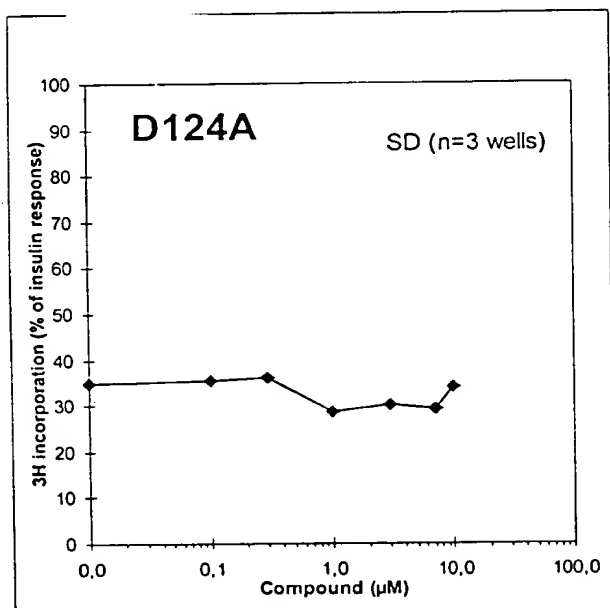
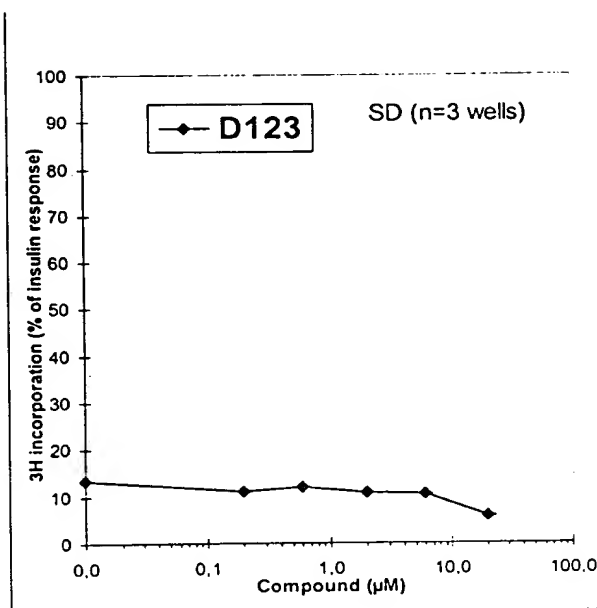


FIGURE 71S2

FIGURE 71T2

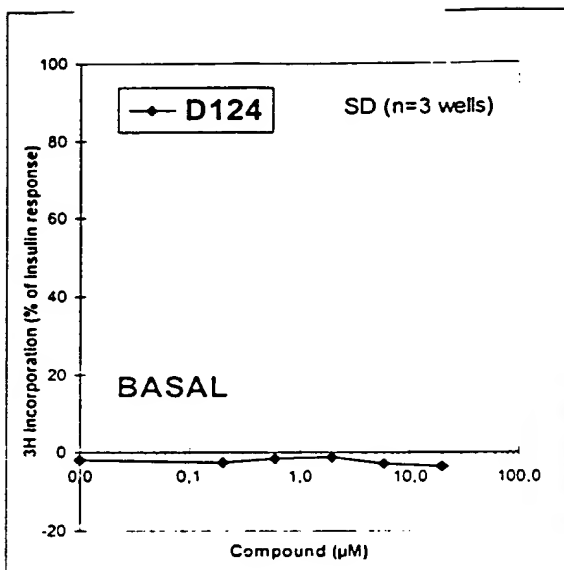


FIGURE 71U2

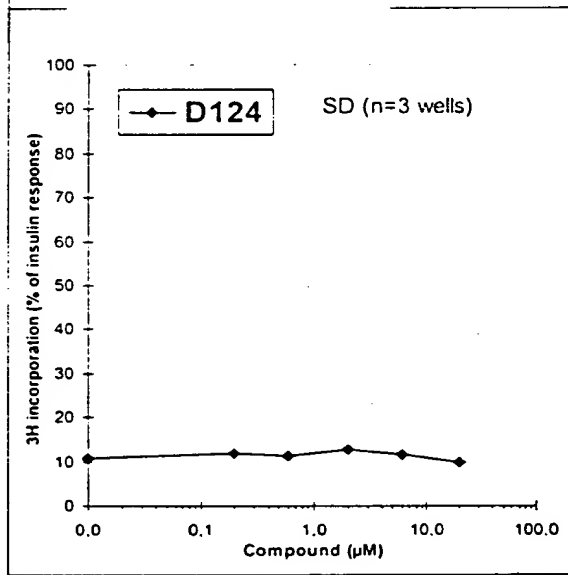
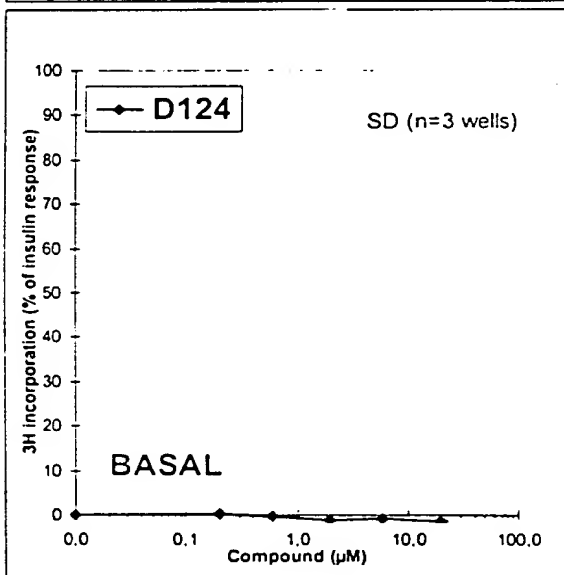
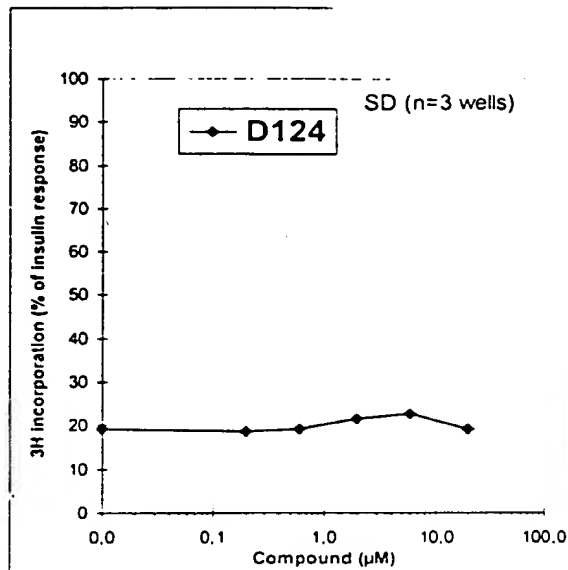


FIGURE 71V2

FIGURE 71W2

FIGURE 71X2

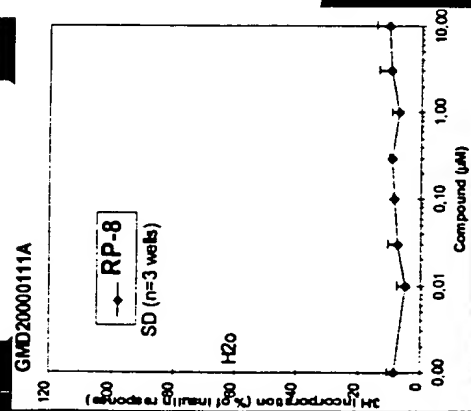


FIGURE 71Y2

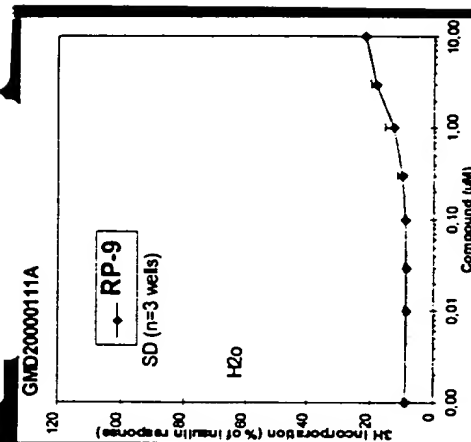


FIGURE 71Z2

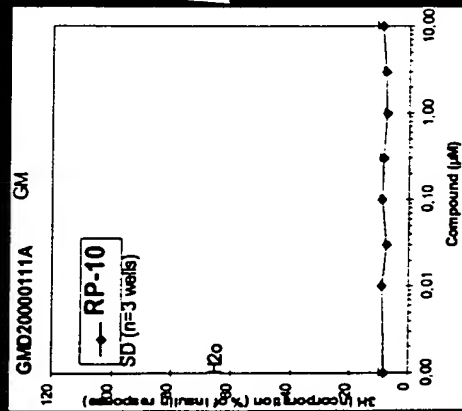
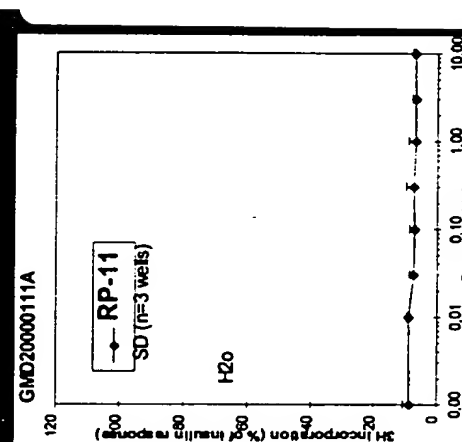
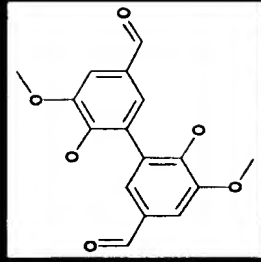


FIGURE 71A3



S291: Dimer of S204 with linker 9

S204 = Lig-GGGFHENFYDWFVRQVSKK



Linker 9 =

HIR binding = 1.2×10^{-6}

FFC:

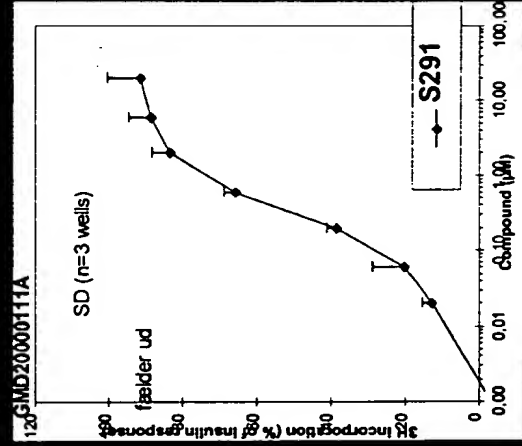


FIGURE 71B3

Figure 1 is a line graph showing the effect of various peptides on the binding of ^{125}I -labeled lacZ to m8p control. The y-axis represents OD 405 (0.2 to 1.2), and the x-axis represents 25000 x binding alone (100% value). The legend includes: Cleaved mono / di-peptide, LFF8, F8 peptide, LFH2C, LFH2C(9)/F8, LFFH2C(6)/F8, LFH2C(12)/F8, and lacZ (m8p control). The control shows a sharp increase in binding at high x-axis values, while the peptides show varying degrees of inhibition.

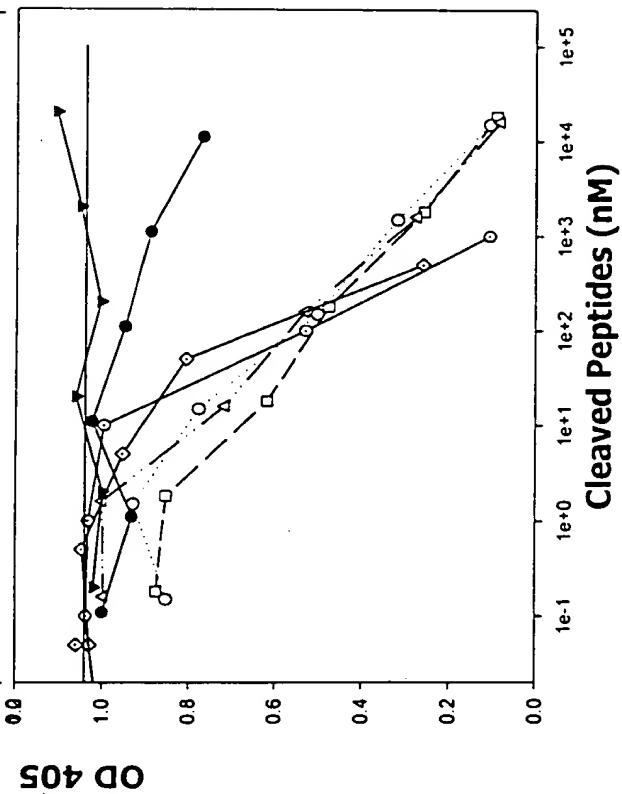


FIGURE 72B

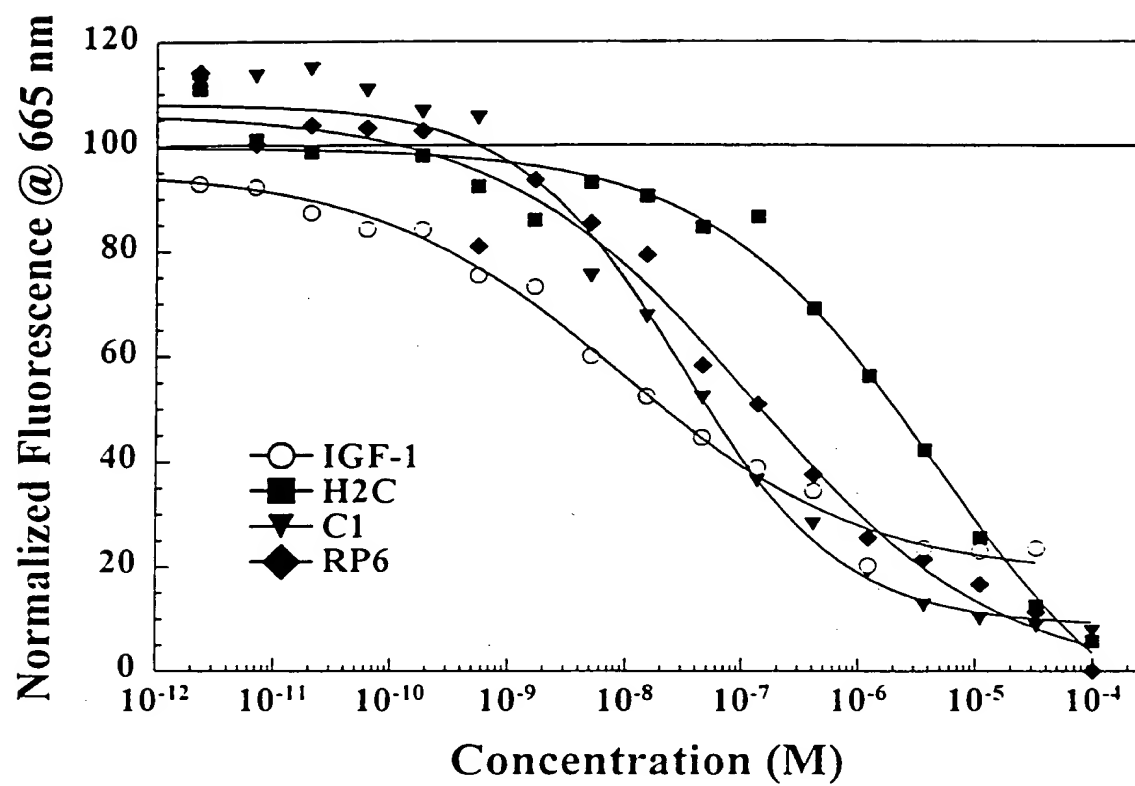


FIGURE 73

FIGURE 74